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July 12, 2004, 14:00:58 ; Search time 50.2093 Seconds (without alignments) 213.658 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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192
1 RRSYRYKLINWAYQQVQNKEDAWIEHDVWRMEI 34
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Maximum Match 100%
Listing first 45 summaries
                                                                             OM protein - protein search, using sw model
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2: sp bacteria:*
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Q9g150 sus scrofa	O924j9 mus musculu	Ogewr7 mus musculu	mus	Q8bwb6 mus musculu	Q99p41 rattus norv	O8ci59 mus musculu	Q924z1 mus musculu	O80zf3 mus musculu	Omor	Q86sf6 homo sapien	homod	Q8iue7 homo sapien	Q7z389 homo sapien	Q8c5f0 mus musculu	
SUMMARIES		di	09GL50	Q924J9	Q9CWR7	Q924Z2	Q8BWB6	Q99P41	Q8CI59	Q924Z1	Q80ZF3	Q9NVB5	Q86SF6	QBNFT2	Q8IUE7	Q7Z389	Q8CSF0	О 8ТDР3
		DB	9	11	11	11	11	11	11	1	11	4	4	4	4	4	11	4
	* Query	Length	338	339	339	339	489	488	488	514	526	488	488	490	490	498	488	456
	* Query	Match	100.0	97.4	97.4	72.4	57.3	56.8	56.8	56.8	56.8	55.7	55.7	55.7	55.7	55.7	54.7	50.3
		Score	192	187	187	139	110	109	109	109	109	107	107	107	107	107	105	96.5
	Result	No.	Н	C/I	е	4	Ŋ	9	7	80	თ	10	11	12	13	14	12	16

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487 4 QBTF03 480 4 QBNEW6 6 480 16 067595 2 366 16 QBA6D0 2 926 1 QBR554 2 1027 5 Q950C7 2 1027 5 Q950C7 2 230 2 Q98PP3 9 556 11 QBCFS 9 556 11 QBCFS 9 556 11 QBCFS 9 556 11 QBCFS 150 12 Q970C4 2 230 2 Q98PP3 9 521 0 Q81PP4 1 1 6 QB1DC 6 1379 5 Q17PP4 1 1 16 QBDSX5 6 1379 1 QBCFS 6 1379 1 QBCFS 6 336 16 QBDBX5 6 336 16 QBCFS 6 336 16 QBCFS 7 00000000000000000000000000000000000	RY; PRT; 338 1. 16, Created) 1. 16, Last sequence othelial antigen of hordata; Craniata; V etartiodactyla; Suinn G., Coupel S., Coulo ou JP., Charreau B pression in endothel vation."; 10. the EMBL/GenBank/ 868 1; -che EMBL/GenBank/ 100.0%; Score 192; 100.0%; Pred. No. 7 ive 0; Mismatche VQQVQNKEDAWIEHDVWRM VQQVNKEDAWIEHDVWRM	PRELIMINARY; PRT; 339 AA. (TrEMBLrel. 19, Created) (TrEMBLrel. 19, Last sequence update)
117 96.5 118 96.5 120 60.5 21 60.5 21 60.5 22 3.2 23 3.2 24 3.1 25 5.5 27 5.5 28 3.0 29 3.1 20 4.0 20 3.1 20 4.0 20 3.1 20 4.0 20 3.1 20 4.0 20 3.1 20 4.0 20 4.0 20 5.5 20 5.5	RESULT 1 Q9GL50 AC D9GL50 DT 01-MAR-2001 (TERBLEL 16, C DT 01-JUN-2003 (TERBLEL 16, L DN Mammalia, Eutheria, Cetartiod ON NCBI_TAXID=982; NN 11 RA Hesland 1-BS-BSD 1-P-P- RA Hesland 1-P- RA H	RESULT 2 Q924J9 ID Q924J9 PRE AC Q924J9; DT 01-DEC-2001 (TY DT 01-DEC-2001 (TX

Length 339;

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Score 187; DB 11;
Pred. No. 3.5e-16;
2; Mismatches 0;
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Mammalia; Eutheria; Rodentia;
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94.1%;
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(TrEMBLrel. 23, I
(TrEMBLrel. 24, I
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Mus musculus (Mouse)
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                        Similarity
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MEDLINE-21085660; PubMed=117851;

Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Komo H., Adachi J., Fukuda S.,

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Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

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Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Winshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Brosseling D., Ring B., Klang K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Whynshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Sciurognathi, Muridae, Murinae, Mus.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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EMBL; AK010437; BAB26938.1; -.
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  01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Six-transmembrane epithelial antigen of the prostate.
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94.1%; Pred. No. 3.5e-16;
ive 2; Mismatches 0;
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Mammalia; Butheria; Rodentia;
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Sciurognathi, Muridae, Murinae, Mus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI TaxID=10090;
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Serru V., Manivet P., Lamblin D., Vaubourdolle M., Kellermann O.,
Loric S.;
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Last annotation update)
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Pred. No. 5.8e-10;
4; Mismatches 5;
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Pred. No. 4.8e-06;
                                                                           185 RRSYRYKILNWAYKQVQQNKEDAWVEHDVWRMEI 218
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MGD; MGI:1921301; 4921538B17Rik.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR004455; NADPoxred F420.
Pfam; PF091807; F420 oxidored; 1.
SEQUENCE 489 AA; 55760 MW; 98CD63D59DD
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Passer B.J., Nancy-Portebois V., Amzallag N., Prieur S., Cans C., Roborel de Climens A., Fiucci G., Bouvard V., Tuynder M., Susini L., Morchisne S.P., Crible V., Lespagnol A., Dausset J., Oren M., Amson R., Telerman A., "The p53-inducible TSAP6 gene product regulates apoptosis and the cell cycle and interacts with Nix and the Myt1 Kinase."; Proc. Natl. Acad. Sci. U.S.A. 100:2284-2289(2003).
                                                                                                                                     Gaps
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodentia, Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Serru V., Lamblin D., Lenoir C., Manivet P., Vaubourdolle P. Kellermann O., Loric S.;
Molecular cloning and expression of mouse dudulin 2.";
Submitted (Br. 2010) 10 the EMBL/GenBank/DDBJ databases.
EMBL; AN029586; ARK50539.1; -.
MGD; MGI:1915678; Tsap6.
MGD; MGI:006618; P:electron transport; IEA.
InterPro; IPRO04455; MADPOxxed F420.
Pfam; PR03807; F420 oxidored; I.
SEQUENCE 514 AA; 57268 MW; 339886C288AEC0EZ CRC64;
                                                                                                                                     Indels
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GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR004455; NADPoxred F420.
Pfam; PF03807; F420 oxidored; I.
SEQUENCE 488 AA; 54749 MW; 9A08D99C90CF83F4 CRC64;
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Last annotation update)
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Last annotation update)
                                                                                           56.8%; Score 109; DB 11; 58.8%; Pred. No. 6.5e-06; iive 5; Mismatches 9;
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58.8%; Pred. No. 6.9e-06;
iive 5; Mismatches 9;
                                                                                                                                                                                             326 RRSHRYDLVNLAVKQVLANKSRLWVEEEVWRMEI 359
                                                                                                                                                                        1 RRSYRYKLINWAYQQVQQNKEDAWIEHDVWRMEI 34
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                                                                                                                                                                                                                                                                                                                                            Created)
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01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                               Local Similarity 58.8 es 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 58.8 es 20; Conservative
                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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Q80ZF3
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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   Gaps
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"Growth inhibition of prostate cancer by an adenovirus expressing a novel tumor suppressor gene, pHyde.";
Cancer Res. 60:4419-4425 (2000).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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 Indels
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-Dunning; TISSUE-Prostatic carcinoma;
In Y., Kinaldy A.R., Steiner M.S.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Steiner M.S., Rinaldy A.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF335281; AAK00361.1; -.
EMBL; AF38865; AAL78207.1; -.
EMBL; AF23865; AAL78207.1; -.
EMBL; AF03807; F420 widored F420.
Pfam; PF03807; F420 widored; I.
SEQUENCE 488 AA: 54640 MW; S9FF07121919FDCB CRC64;
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Straumberg R.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC037435; AAH37435.1; -.
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Pred. No. 6.5e-06;
5; Mismatches 9;
                                                            325 RRSERYLFINMAYQQVHANIENAWNBEEVWRIEM 358
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                                     1 RRSYRYKLINWAYQQVQQNKEDAWIEHDVWRMEI 34
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                                                                                                                                                                      488 AA
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STRAIN-Dunning; TISSUE-Prostatic carcinoma;
MEDLINE-20424188; PubMed=10969787;
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Mismatches
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01-MAR-2003 (TrEMBLrel. 23, Last seque
01-MAR-2003 (TrEMBLrel. 25, Last annot
similar to RIKEN DNA 1010001D01 gene.
                                                                                                                                                                                                           Created)
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Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                   Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
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01-JUN-2003
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21;
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Q8CIS9

RESULT 7
08C159
11D 08C159
11D 01-M
DT 01-M
DT 01-O
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Matches

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A Passer B.J., Nancy-Portebois V., Amzallag N., Prieur S., Cans C.,
Roborel de Climens A., Flucci G., Bouvard V., Tuynder M., Susini L.,
A Morchoisne S.P., Cribbe V., Lespagnol A., Dausset J., Oren M.,
Amson R., Telerman A.;
Telerman A.;
Telerman A.;
Trep p53-inducible TSAP6 gene product regulates apoptosis and the cell
RT cycle and interacts with Nix and the Mytl kinase.";
Proc. Natl. Acad. Sci. U.S.A. 100:2284-2289(2003).
BMBL; BC042150; AAH42150.1; -.
BMBL; AV21461; AA038238.1; -.
RGO, GO:0006118; P:electron transport; IEA.
InterPro; IPR004455; NADPoxred F420.
R fam; PF03807; F420 oxidored; T.
RPOSITE; PS00220; IG MHC; 1.
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"Cloning and characterization of a novel six-transmembrane protein STEAP2, down-regulated in androgen-independent prostate cancer."; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF455138; AAN04080.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                             Strausberg R., submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
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01-ocr-2002 (TrEMBLrel. 22, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Six-transmembrane epithelial antigen of prostate 2.
STEAP2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.7%; Score 107; DB 4; 55.9%; Pred. No. 1.2e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.7%; Score 107; DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RRSYRYKLINWAYQQVQQNKEDAWIEHDVWRMEI 34
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0006118; P:electron transport; IEA.
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Pfam; PF03807; F420_oxidored; I.
Transmembrane.
                                                                                                 SEQUENCE FROM N.A. MEDLINE=22506415; PubMed=12606722;
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    TISSUE=Kidney;
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Q8IUE7;
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ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Naqai K., Sugano S., Aotsuka S., Yoshikawa Y.,
Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,
Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;
"NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

Serru V., Manivet P., Lenoir C., Eschwege P., Lamblin D.,
Vaubourdolle M., Kellermann O., Loric S.;
Vaubourdolle M., Kellermann O., Loric S.;
Ubdulin 2, a new tumor antigen expressed in various human tumors.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AK001691; BAA91839.1;
EMBL, AV029585; AAK55038.1;
EMBL, AV029585; ARX5038.1;
InterPro, IPR003006; Ig MHC.
InterPro, IPR004055; NADPoxxed F420.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                       Length 526;
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                                                                                                                                                                         Indels
GO; GO:0006118; P:electron transport; IEA.
InterPro: IPR04455; NADPoxred F420.
Pfam; PF03807; F420. oxidored; I.
SEQUENCE 526 AA; 58530 NW; 6306CD717E25200A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 24, Last annotation update)
Hypotherical protein FLJ10829 (Budulin 2).
Homo sapiens (Human):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to dudulin 2 (TSAP6).
                                                                                                                                                                         9;
                                                                                                                       Score 109, DB 11;
Pred. No. 7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 107; DB 4;
Pred. No. 1.2e-05;
6; Mismatches 9;
                                                                                                                                                                                                                                                  364 RRSHRYDLVNLAVKQVLANKSRLWVEEEVWRMEI 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   326 RRAHRYDLVNLAVKQVLANKSHLWVEEEVWRMEI 359
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                                                                                                                       56.8%;
                                                                                                                                                                       20; Conservative
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Matches 19; Conser
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                                                                                                                       Query Match
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Q86SF6;
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490 AA

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490 AA

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rSAP6 OR 1010001D01RIK.
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                                                                                                                                                                                     Saatcioglu F.; "Molecular cloning and characterization of STAMP1, a highly prostate specific six-trans-membrane protein that is overexpressed in prostate
                                                                                                                                                                                                                                                                                                                                                                             Gaps
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TISSUB-Human colon endothel primary cell culture;
TISSUB-Human colon endothel primary cell culture;
Bloecker H., Boechen M., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX538047, CAD97986.1; -.
Hypothetical protein.
SEQUENCE 498 AA; 55593 MW; 69DD23D5A00C2D6B CRC64;
                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.2e-05;
6; Mismatches 9; Indels
                                                                                                                                            TISSUE=Prostate;
MEDLINE=22229309; PubMed=12095985;
Korkmaz K.S., Elbi C.C., Korkmaz C.G., Loda M., Hager G.L.,
                                                                                                                                                                                                                                                                                                                                              55.7%; Score 107; DB 4; Length 490;
58.8%; Pred. No. 1.2e-05;
ive 5; Mismatches 9; Indels
                                                                                                                                                                                                                                         J. Biol. Chem. 277:36689-36696 (2002).

BMBL; AXO08445; AAG32149.1; -.
GO; GO:0006118; P:electron transport; IEA.

InterPro: IPRO04455; NADPoxred F420.

Pfam; PF03807; F420 oxidored; I.

SEQUENCE 490 AA; -56027 MW; D1971A84880F7E51 CRC64;
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Last sequence update)
Last annotation update)
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein DKFZp686H07150.
DKFZP686H07150.
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Best Local Similarity 55.99
Matches 19; Conservative
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hes 20; Conservative
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                                                          Homo sapiens (Human)
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                                                                                                                             SEQUENCE FROM N.A.
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01-JUN-2003 (Treme
DUDULIN 2 homolog.
                                                                                                  NCBI_TaxID=9606;
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 01-MAR-2003
                                                                                                                                                                                                                               cancer.";
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Q7Z389
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ID Q8C5F
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MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:6553-573(2002).
EMBL; AK078769; BAG73783.1; -.
MGD; MGI:1915678; Tsap6.
GO; GO:0066118; P:electron transport; IRA.
InterPro; IPR004455; NADPOARCE F420.
Ffam; PF03807; F420 oxidored; I.
SEQUENCE 488 AA; 54780 WW; FDFC4F42AE503D11 CRC64;
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                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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58.8%; Pred. No. 2.1e-05;
tive 4; Mismatches 10;
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Matches 20; Conservative
Mus musculus (Mouse)
                                                                                                                        [1]
SEQUENCE FROM N.A.
                                                                                       NCBI_TaxID=10090;
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Search completed: July 12, 2004, 14:10:25 Job time : 51.2093 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

July 12, 2004, 13:52:02; Search time 10.6744 Seconds (without alignments) 165.853 Million cell updates/sec Run on:

US-10-010-667A-2_COPY_185_218 192 1 RRSYRYKLIAWAYQQVQQNKEDAWIEHDVWRMEI 34 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	09uhe8	caeno	P46918 bacillus su	Q8d3c0 wiggleswort			P27715 caenorhabdi		Q9lik7 arabidopsis			rattı	Q9upn3 homo sapien	homo	baci	P57323 buchnera ap			Q9z987 chlamydia p	xylella	Q87ds1 xylella fas			homo	O35136 mus musculu	bos t		Q97z79 sulfolobus	_	Q10216 schizosacch		_	Q8g4v2 bifidobacte
SUMMARIES	ID	TEA HUMA	CE11 CAEEL	GGAB_BACSU	SYT WIGBR	Y4BJ RHISN	YOKC BACSU	UN13 CAEEL	GLPK_SYNY3	ACAD ARATH	TRUB PROMA	ALP4 SCHPO	SYJ1_RAT	MACF HUMAN	MAC4 HUMAN	YQ04_BACAN	DAPD BUCAI		OXAA_CHLTR	SYV CHLPN	TRUA XYLFA	TRUA XYLFT	GLPK ANASP	Y4WA_RHISN	NCM2 HUMAN	NCM2 MOUSE	SYJ1 BOVIN	SYJ1 HUMAN	IF2A SULSO	MO2L CAEEL	YAY8 SCHPO	ASSY_PSEPK	SYN SHEON	SYR_BIFLO
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AGLU MUCJA ENV ČAEVG	FTSK VIBPA O16G BACSU	DHG_ECOLI	CYGF_BOVIN VAB1_CAEEL	TRMD_CAUCR VATA_HALVO	PEPX_RHOBA VPS5_YEAST
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864 942	1028 561	796	1103	245 586	626 675
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4 4 8 8	48	47.5	47.5	47	47

ALIGNMENTS

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WormPep; ZK512.3; CE00409. InterPro; IPR002111; Cat_channel_TrpL. SEQUENCE 1418 AA; 159237 MW; 4FC83B9E7ADF7788 CRC64;

PIR; S40764; S40764.

SARRA

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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Rooper A., Saunders B., Shownken R.,
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer B., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                    GO; GO: 0005887; C:integral to plasma membrane; TAS.
GO; GO: 0005911; C:intercellular junction; TAS.
GO; GO: 0015567; F:channel/pore class transporter activity; TAS.
Transmembrane; Antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                      Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
55443A170C870387 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 192; DB 1; 100.0%; Pred. No. 5.8e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 RRSYRYKLINWAYQQVQQNKEDAWIEHDVWRMEI 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RRSYRYKLINWAYQQVQQNKEDAWIEHDVWRMEI 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1418 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                    entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                              POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                   EMBL; AF186249; AAF17479.1; -.
EMBL; AC005053; AAC79150.1; ALT_INIT.
EMBL; AC004969; AAD15620.2; -.
EMBL; BC011802; AAH11802.1; -.
Genew; HGNC:11378; STEAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Bristol N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                39851 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ced-11 protein.
CED-11 OR ZK512.3.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                291 3
339 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1] -
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                     34;
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P34641;
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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EMBL; Z22177; CAA80145.1; -.

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RA Kunst F. Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brouilet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouilet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouilet S., Brington J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Brouilet S., Devine K.M., Dusterhoff A., Ehrlich S.D., Emmerson P.T.,
RA Britz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron N.,
RA Ghims S.Y., Glaser P., Goffeau A., Golightly E.J., Garadi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Haga K., Haiech J., Harwood C.R., Itaya M., Jones I.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Kocheter P., Kohingstein G., Krogh S., Kumano M.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sachote F.,
Sakiguchi J., Scanlan E., Schleich S., Schroceter R., Scoffone F.,
RA Takeuchi M., Tamakoshi A., Tarkahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaafa T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaafa T., Takahashi H., Weitzenegger T.,
RA Takati A., Wanbutt R., Wedler E., Wanbue K., Yasumoto K., Yata K.,
Voshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
R. The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: Involved in the biosynthesis of galactosamine-containing minor teichoic acid, a non-essential cell wall polymer in B.subtilis 168.
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PATHWAY: Poly(glucopyranosyl N-acetylgalactosamine 1-phosphate) teichoic acid biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Preymond F.-P., Karamata D.;
Sequenching and analysis of two gga genes associated with the
"Yathhesis of the minor teichoic acid of Bacillus subbtilis 168.";
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
                                             3,
    Score 58.5; DB 1; Length 1418; Pred. No. 5.5;
                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                             5,
                                                                                                                                                                                                                                                       (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                 Minor teichoic acid biosynthesis protein ggaB.
                                           5; Mismatches
                                                                                                     1355 EVAENENDTDNAWTEHDVWAISL 1377
                                                                               15 OVOONKED---AWIEHDVWRMEI 34
                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98044033; PubMed=9384377;
    30.5%;
Query Match
Best Local Similarity 43.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 390:249-256(1997).
                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                           Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                            GGAB OR BSU35680.
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1423;
                                                                                                                                                                                                                                                           01-NOV-1995
01-NOV-1995
                                                                                                                                                                                                                                                                                                     10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=168;
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BACSU
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InterPro; IPR006195; tRNA ligase II
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Best Local Similarity
                                                                                                                                                                                          242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI TaxID=394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y4BJ RHISN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
SEQUENCE
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Matches
                                                                                                                                                                                             DOMAIN
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Y4BJ_RHISN
                                                                                                                                                                                                                                                                   METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
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                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profift institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diphosphate + L-threomyl-tRNA(Thr).
-!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
-!- SUBUNIT: Homodimer (By sullarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ξ.
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Akman L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wigglesworthia glossinidia brevipalpis.
Bacteria, Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Wigglesworthia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome sequence of the endocellular obligate symbiont of tsetse
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Threonyl-tRNA synthetase (EC 6.1.1.3) (Threonine--tRNA ligase)
                                                                                                                                                                                                                                     EMBL; U13979; AAA73513.1; -.

EMBL; Z99122; CAB15585.1; -.

EMBL; Z99121; CAB15585.1; -.

Subtinist; BG1192; ggab.

InterPro; IPR001173; Glyco_trans_2.

InterPro; IPR007554; Glyphos_transf.

Pfam; PF00555; Glycos_transf.

Pfam; PF04464; glyphos_transf.; 1.

Teichoic_acid_biosynthesis; Transferase; Glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             flies, Wigglesworthia glossinidia.";
Nat. Genet. 32:402-407(2002)
-!- CATALYTIC ACTIVITY: ATP + L-threonine + tRNA(Thr) = AMP
  SIMILARITY: Belongs to the glycosyltransferase family 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.2%; Score 58; DB 1; Length 900; 33.3%; Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107154 MW; FA66495488C2C62F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||:|:|:| : :| | : :||| 591 RSFRHKILTLSSSKVISTHADIWVVNPFFNMEI 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 RSYRYKLINWAYQQVQQNKEDAWIEHDVWRMEI 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          636 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAMAP; MF_00184; -; 1.
InterPro; IPR004154; HGTP_anticodon.
InterPro; IPR004314; tRNA-synt_2b.
InterPro; IPR002320; tRNA-synt_thr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell wall; Complete proteome
SEQUENCE 900 AA; 107154 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYT WIGBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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pfam; pF03129; HGTP_anticodon; 1.
pfam; pF00389; FRNA_SYNT E.D; 1.
PRINTS; PR01047; TRNASYNTHTR.
TIGREAMs; TIGR00418; thrs; 1.
PROSTITS; PSSOB62; AA FRNA_LIGASE II; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding; Metal-binding; Zinc; Complete protecome.
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MEDLINE=97305956; PubMed=9163424;
Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NATURE 387:334-401[1997].
-!-SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!-SIMILARITY: DISTANTLY RELATED TO PEPTIDASE FAMILY S2C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular basis of symbiosis between Rhizobium and legumes.";
                                                                                                                                                                                                                   (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                     Score 54.5; DB 1; Length 636; Pred. No. 7.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria, Proteobacteria, Alphaproteobacteria; Rhizobiales, Rhizobium/Agrobacterium group, Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 630;
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                                                                                                                                                                                                                                                                                                75381 MW; 6B5695AE61D57F7E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 8
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1. Similarity 35.5%; Pred. No. 9.1;
11; Conservative 5; Mismatches
                                                                                                                                                                                                                   ZINC (CATALYTIC)
ZINC (CATALYTIC)
ZINC (CATALYTIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; Plasmid; Transmembrane.
TRANSMEM 8 28 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              630 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      281 RKKLKKFYYQEV---KTPCIIDHDLWRL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 RYKLLNWAYQQVQQNKEDAWIEHDVWRM 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (or send an email to license@isb-sib.ch)
                                                                                                                                                                                                CATALYTIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEROPS; SO1.UPC; -.
InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001940; Peptidase_S1C.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Last annotat
Hypothetical 67.9 kDa protein Y4BJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE000066; AAB91625.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67854 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhizobium sp. (strain NGR234)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00834; PROTEASES2C
                                                                                                                                                                                                                                                                                                                                                              28.4%;
                                                                                                                                                                                                                                                                                                                                                                                  42.9%;
                                                                                                                                                                                                                                                                                                                                                           Query Match 28.4
Best Local Similarity 42.9
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                      333
384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid sym pNGR234a
                                                                                                                                                                                                                   333 3
384 3
510 5
636 AA;
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Complete proteome. 17 MW; 34852BDAEA4805D2 CRC64;

protein; Complet 9 AA; 9287 MW;

79 AA;

Hypothetical

SEQUENCE

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S K
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                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RA Kunst F. Ogasawara N., Moszer I., Albertini A.M., Alloni G., RA Aunstersovity S. A. Kunst F. C. Ogasawara N. Gordoni A., Bortin A., Borchert S., Raevedo V., Bertero M.G., Bessiezes P., Bolotin A., Borchert S., Azevedo V., Bertero M.G., Bessiezes P., Bolotin A., Borchert S., Raburitss R., Bursier L., Brans A., Braun M., Erighell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Dentiatot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., Ra Britan K.D., Errington J., Fabret C., Ferrari E., Poulger D., Ra Ghima S.Y., Glaser P., Goffeau A., Golightly B.J., Grandi G., Guiseppi G., Guy B.J., Hagager K., Hastoch J., Harwood C.R., Henaut A., R. Guiseppi G., Guy B.J., Hagage K., Haicch J., Harwood C.R., Henaut A., R. Aulbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones I., R. Vobasahi Y., Koetter P., Koningstein G., Kroph S., Kumano M., Kurita K., Lapidus A., Lardinois S., Laudber J., Lazarevic V., R. Mediau A., Liu H., Masuda S., Mauel C., Medigue C., Mediau N., Mellado R.P., Marzuno M., Moestl D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Presecan B., Pulc P., Purnelle B., Rapoport G., Rey M., Reynolds S., Schroeter R., Scoffone F., Schleich S., Schroeter R., Scoffone F., Schleich S., Schroeter R., Scoffone F., Seriguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Sorokin A., Tanakoshi H., Tanakoshi H., Tanakoshi H., Tanakoshi H., Tankanato K., Walmoute K., Walmoute K., Walmoute R., Walmanoto K., Yata K., Willer R., Walmanoto K., Yata K., Willer R., Walmanoto K., Yata K., Walmanoto M., Walmiers P., Wipat A., Yamamoto H., Yamamoto K., Yasumoto K., Yasumoto K., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Sunberling R., Weller H., Walmanoto K., Walmin R., Schroeter M., Walmanoto K., Walmoto M., Wall R., Walmanoto K., Walmoto M., Walmanoto M., Walmanoto M., Walmanoto M., Walmanot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Systematic sequencing of the 283 kb 210 degrees-232 degrees region of the Bacillus subtilis genome containing the skin element and many
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mizuno M., Masuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M., Kobayashi Y.,
                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                              Last sequence update)
Last annotation update)
296 RRYYRRELFGWEYR-----AKLEPEIWR 318
                                                                                                                        79 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97124195; PubMed=8969508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Microbiology 142:3103-3111(1996).
                                                                                                                                                                01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last seq
10-0CT-2003 (Rel. 42, Last ann
Hypothetical protein yqkC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; 299116; CAB14297.1; -. PIR; E69966; E69966.
SubtiList; BG11758; yqkC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D84432; BAA12635.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 390:249-256(1997).
                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                     FROM N.A.
68 / JH642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sporulation genes."
                                                                                                                                                                                                                                                                                      Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=168;
                                                                                                                                                                                                                                                                    TOKC OR BSU23650
                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=168 /
                                                                                                                   YOKC BACSU
P54566;
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                               YOKC_BACSU
                                                                      RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maruyama I.N., Brenner S., "A phorbol ester/diacylglycerol-binding protein encoded by the unc-13 gene of Caenorhabditis elegans."; Proc. Natl. Acad. Sci. U.S.A. 88:5729-5733(1991).
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        functions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDITINE 33075060, PubMed=1445255;
Ahmed S., Maruyama I.N., Kozma R., Lee J., Brenner S., Lim L.,
Ahmed S., Maruyama I.N., Kozma R., Lee J., Brenner S., Lim L.,
are Caenorhabditis elegans unc-13 gene product is a phospholipid-
dependent high-affanity phorbol ester receptor.";
Biochem. J. 287:995-999 (1992).
-!- FUNCTION: May form part of a signal transduction pathway,
transducing the signal from diacylglycerol to effector functions
One such function could be the release of neurotransmitter from
                                                                                                                                                                                                   UN13 CAEEL STANDARD;
PRT; 1813 AA.
97715; 0.17665; 0.23312; 0.81695;
01-AUG-1992 (Rel. 23, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
1-0.607-2003 (Rel. 42, Last annotation update)
Phorbol ester/diacylglycerol-binding protein unc-13 (Uncoordinated protein 13).
                                         0;
Score 52; DB 1; Length 79;
Pred. No. 1.7;
8; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Bristol N2, Gardner A.E., Lloyd C.R.; Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=4; Synonyms=ZK524.2b;
IsoId=P27715-4; Sequence=VSP_004486, VSP_004487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=5;
Name=1; Synonyms=ZK524.2a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PARTIAL SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
                                                                                               23 QNHPYTLLHWSIGGAESIKKDVWLLQDEMTFE 54
                                                                            2 RSYRYKLLNWAYQQVQQNKEDAWIEHDVWRME 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=P27715-2; Sequence=VSP_004484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=P27715-3; Sequence=VSP_004485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=1; Synonyms=ZK524.2a;
IsoId=P27715-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REVISIONS, AND ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nervous system.";
Mol. Biol. Cell 11:3441-3452(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Bristol N2;
MEDLINE=91288538; PubMed=2062851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZINC AND PHORBOL-ESTERS BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 2).
                    28.1%;
   27.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neurons.
ALTERNATIVE PRODUCTS:
                                         Conservative
                                                                                                                                                                                                                                                                                                                               UNC-13 OR ZK524.2.
Caenorhabditis elegans.
                 Local Similarity
nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=2
 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Durbin R
                                                                                                                                                                                      CAEEL
                                      Matches
                                                                                                                                                                   RESULT
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                                                                                                                                                                                                         /FTIG=VSP_004487.

A -> ATLQ (in isoform 5).
/FTIG=VSP_007342.

I -> LVLK (IN REF. 1).
VUKADNFPQTSEHTKFSNS -> CRQADTSHKHQNTQILEH
                                                                                      ASPODHYHRSDSTAQOPGNNI VRQTIQEEEKRNYQELWH
WYKKVKADAGI -> MRYPSELAYDRASPEYLNSDPSRY
SPNÇOLKRSTYRIKSYEDRNGGRERI YTTKLVSVYLEKMR
PPDELEEGSSGSMRETQNEIKNGTQLHNAESNIFFPQDSVP
                                                                                                                                           KSISYNAGNLKNTSITTSKTSSAITNHSSLPPQPPSKPASR
DSDPMKQLLTFSKSFKKVRRVRSAMPRRRKRKRVKIKKSRS
CPILMKTEKTPHPMKSKSNTCIRIPKKTVIAPLRKEIKIVR
                                                HIRTGANTWREPSTSSRPTSSQAWNYQDDTHQYDEVDRGSR
VSFTRTPSVDRTDRPSESGGGFYDEMSESGRPGRPDSHNW
RYDSIQEEDNEKDNWKQHVEGYEGGEEKQKDNQKPNDHSA
                       RDEPILEHS<u>E</u>PEYVYDQNGYPEEDNYGINPTYSEDHFEGQT
NDYSTTHQEPNDFRNDYNSSYQREYWNESBPLSYNSRPPNG
                                                                                                                                                                                 MKPPAARCESDSKAHKKKNLLDVYKDMG (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97061201; PubMed=8905231; Ranaka A., Asamizu E., Nakamura Y., Kaneko T., Sato S., Kotani H., Tanaka A., Asamoto S., Kimura T., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Chanara M., Yasuda M., Tabata S., "Sequence analysis of the genome of the unicellular cyanobacterium synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           metabolism.
-!- CATALYTIC ACTIVITY: ATP + glycerol = ADP + glycerol 3-phosphate.
-!- PATHWAY: Glycerol utilization; rate-limiting step.
-!- SIMILARITY: Belongs to the fucokinase / gluconokinase / glycerokinase / xylulokinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glycerol kinase (RC 2.7.1.30) (ATP:glycerol 3-phosphotransferase)
                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 1813;
                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                               649D1B39F18ACFD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                    5;
                                                                                                                                                                                                                                                                                             (IN REF. 1).
I -> N (IN REF. 1)
V -> A (IN REF. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       495 AA
                                                                                                                                                                                                                                                                                                                                                                      56;
                                                                                                                                                                                                                                                                                                                                                                                  5; Mismatches
                                                                                                                                                                                                                                                                                                                                                        Score 52;
Pred. No. 5
                                                                                                                                                                                                                                                                                          (IN REF. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                             || | :|: |::| :|
511 NWRYDSIQEEDNEKDNWKQH 530
                                                                                                                                                                                                                                                                                                    1531 1531 I ->
1648 1648 V ->
1813 AA; 207250 MW;
                                                                                                                                                                                                                                                                                                                                                                                                              10 NWAYQQVQQ--NKEDAWIEH 27
                                                                                                                                                                                                                                                                                                                                                         27.1%;
40.0%;
                                                                                                                                                                                                                                                                                                                                                                                     8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                647
1305
348
                        909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycerol kinase (EC (Glycerokinase) (GK) GLPK OR SLR1672.
                                                                                                                                                                                                                                                                                                                                                                      Similarity
                        349
                                                                                                                                                                                                                                                                647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLPK SYNY3
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                     CONFLICT
                        VARSPLIC
                                                                                                                                                                                                                         /ARSPLIC
                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                 SEQUENCE
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P74260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLPK_SYNY3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MDDVGDYNDDQLSDGMSMRILCITIKKARLQGAVDEFNSYV
TVKLQTVKSTTVAVRGNLPCWEQBFIFETNRPDDGMVLELW
         Name=5; Synonyms=ZK524.2c;
Isold=P27715-5; Sequence=VSP_007342;
Note=No experimental confirmation available;
DOMAIN: The phorbol ester binding activity is zinc and calcium-
                                                                             MISCELLANEOUS: Mutations in unc-13 cause diverse nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3P_004484.
(in isoform 3).
Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /FTId=VSP 004484.
Missing (in isofc/FTId=VSP 004485.
                                                                                                                                 -!- SIMILARITY: Contains 3 C2 domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR, A41101; A41101.
PIR, T19295; T19295.
PIR, T197866; T27886.
HSSP; P28867; TPT0.
WormPep, ZK524.2a; CE15371.
WormPep, ZK524.2c; CE35371.
WormPep, ZK524.2c; CE32552.
InterPro; IPR000008; C2.
InterPro; IPR000973; C2 Calls.
InterPro; IPR00219; DAG PE-bind.
Pfam; PF00186; C2; 3.
Pfam; PF00130; DAG PE-bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                            JOINED.
                                                                                                                                                                                                                                                                                                                                                                       JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Z73912; CAD56561.1; JOINED. Z73912; CAD56619.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Z79694; CAD56619.1; JOINED. Z92779; CAD56619.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Z79694; CAD56561.1; JOINED
                                                                                                                                                                                                                                                                                                         CAB07173.1; -.
CAB07173.1; JOINED
                                                                                                                                                                                                                                                                                                                                 CAB07173.1; JOINED
                                                                                                                                                                                                                                                                EMBL; M62830; AAA93094.1; -. EMBL; U50735; AAA99780.1; -.
                                                                                                                                                                                                                                                                                           AAA99781.1; -.
                                                                                                                                                                                                                                                                                                                                                         CAA98147.1; -CAA98147.1; J
                                                                                                                                                                                                                                                                                                                                                                                                                                       CAD56559.1;
CAD56559.1;
CAD56559.1;
                                                                                                                                                                                                                                                                                                                                              CAA98146.2;
                                                                                                                                                                                                                                                                                                                                                                                                   CAB01966.1;
                                                                                                                                                                                                                                                                                                                                                                                                              CAB01966.1;
CAB01966.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAD56561.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15
                                                                                                                                                                                                                                                                                         US0735; 7
Z92779; 0
Z79694; 0
Z73912; 0
Z73912; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                       Z79694;
Z92779;
Z73912;
Z92779;
                                                                                                                                                                                                                                                                                                                                                                       Z79694;
Z92779;
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Z73912;
                                                                  dependent
                                                                                                                                                                                                                                                                                                                                                                                                   Z79694;
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                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                         EMBL;
EMBL;
EMBL;
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1;

Gaps

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EMBL; AP001300; BAB03036.1; -.
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  entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- ENZYME REGULATION: Activated by calmodulin (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- DOWAIN: The N-terminus contains an autoinhibitory calmodulin-binding domain, which binds calmodulin in a calcium-dependent fashion (By similarity).
-!- SIMILARITY: Belongs to the cation transport ATPases family (P-type ATPases). Subfamily IIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BAC clones.";
Res. 7:217-221 (2000).
Res. 7:217-221 (2000).
FUNCTION: This magnesium-dependent enzyme catalyzes the hydrolysis of ATP coupled with the translocation of calcium from the cytosol out of the cell or into organelles (By similarity).

CATALYTIC ACTIVITY: ATP + H(2)O + Ca(2+) (Cis) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots, rosids;
eurosids II, Brassicales; Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=cv. Columbia;
MEDLINE=203861099; PubMed=10907853;
MEDLINE=203861099; PubMed=10907853;
Kaneko T., Katoh T., Sato S., Nakamura A., Asamizu E., Tabata S.;
"Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the 4,251,695 bp regions covered by 90 Pl, TAC DNA Res. 7:217-221 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Potential calcium-transporting ATPase 13, plasma membrane-type
(EC 3.6.3.8) (Ca(2+)-ATPase isoform 13).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 51; DB 1; Length 495;
Pred. No. 18;
7; Mismatches 10; Indels
                                                                                                                   HSSP; P08859; IGLC.

HAMALP, MF 00186; -; 1.

InterPro; IPR000599; Glycerol_kin.

InterPro; IPR005999; Glycerol_kin.

Fram; PF00370; FGGY_C; 1.

Pfam; PF00370; FGGY_C; 1.

TGRFAMS; TIGRO1311; Glycerol_kin; 1.

PROSITE; PS00493; FGGY_KINASES_1; FALSE_NGC.

PROSITE; PS00445; FGGY_KINASES_2; 1.

Glycerol_metabolism; Transferase; Kinase; ATP-binding; Nomplete protecome.
                                                                                                                                                                                                                                                                                                                                                                                                 ATP (PROBABLE).
71AAC71E76816736 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 YEGNIVGQAYKELTQFYPKAGWVEHDALEIWR 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 YRYKLLINWAYQQVQQNKEDA-WIEHD---VWR 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1017 AA
                                                                                                                                                                                                                                                                                                                                                                                                                        495 AA; 54351 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 34.4%;
11; Conservative
                                                                       EMBL; D90913; BAA18354.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                 168
                                                                                                 S75895; S75895.
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Matches 11; Conserv
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10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
tRNA pseudouridine synthase B (EC 4.2.1.70) (tRNA pseudouridine synthase) (Psi55 synthase) (Pseudouridylate synthase) (Uracil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                         TIGRPAMS; TIGRO1517; ATPASS-IIB Ca; 1.
TIGRPAMS; TIGRO1494; ATPASS P-type; 5.
PROSITE; PSO0154; ATPASE E1 E2; 1.
Hydrolase; Calcium transport; Transmembrane; Phosphorylation; ATP-binding; Metel-binding; Magnesium; Calmodulin-binding; Multigene family; Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CALMODULIN-BINDING (PROBABLE).
PHOSPHORYLANION (BY SIMILARITY)
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcacea;
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112527 MW; 2F0265CCE8862916 CRC64;
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CYTOPLASMIC (POTENTIAL)
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LUMENAL (POTENTIAL).
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LUMENAL (POTENTIAL).
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HSSP; P04191; 1EUL.
InterPro; IPR005408; ATPase =11B Ca.
InterPro; IPR00177; ATPase =1-E2.
InterPro; IPR00177; ATPase =1-E2.
InterPro; IPR00608; Cation_ATPase_N.
InterPro; IPR008250; B1-E2 ATPase_N.
InterPro; IPR005834; Hydrolase_Pfam; PF00689; Cation_ATPase_C.
Pfam; PF00689; Cation_ATPase_C; 1.
Pfam; PF00122; B1-E2 ATPase_N; 1.
Pfam; PF00122; B1-E2 ATPase, 1.
Pfam; PF001029; Cation_ATPase_N; 1.
Pfam; PF001029; Hydrolase; 1.
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SEQUENCE FROM N.A.
STRAIN=SARG / CCMP 1375 / SS120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.6%;
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nes 9; Conserv
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NCBI_TaxID=1219;
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SYJ1 RAT
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"The fission peak gamma-tubulin complex is required in G(1) phase and
is a component of the spindle assembly checkpoint.";
EMBO J. 19:6098-6111(2000).
MEDLINE=22810154; PubMed=12917486;
Dufresne A., Salanoubat M., Partensky F., Artiguenave F., Axmann I.M., Barbe V., Duprata S., Galperin M.Y., Koonin E.V., Le Gall F., Makarova K.S., Ostrowski M., Ostas S., Robert C., Rogozin I.B., Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P., Wolf Y.I., Hess W.R., yanobacterium Prochlorococcus marinus SS120, a nearly minimal oxyphototrophic genome.", Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025(2003).

-: FUNCTION: Responsible for synthesis of pseudouridine from uracil-55 in the psi GC loop of transfer RNAs (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to the pseudouridine synthase truB family. Subfamily 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-0cT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Spindle pole body component alp4 (Altered polarity protein 4).
ALP4 OR SPRC365.15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 313;
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TRNA processing; Lyase; Complete proteome.
ACT SITE 42 42 BY SIMILARITY.

SENTENNER 313 AA: 35024 MW; 34EF5DEB05FF172B CRC64;
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Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
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HAMAP; MF_01080; -; 1.
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Best Local Similarity 42.3%;
Matches 11; Conservative '
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09Y705;
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GN ALP4 OF
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An Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton U., Simmonds M., Squares R., Squares S., Stevens K., Taylor K.G., Tivey A., Walsh S.V., Warren T., Whithehead S., Wodward J., Volckaert G., Aert R., Robben J., Grymonpiez B., Wodward J., Volckaert G., Aert R., Robben J., Grymonpiez B., Ameljens I., Vanstreels E., Rieger M., Scheefer M., Meeller H., Rabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., B. Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., B. Berz P., Zimmermann W., Wedler H., Wambult R., Purnelle B., A. Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., A. Loss M., Kochet M., Gallardin C., Tallada V.A., Galzon A., Thode G., Dominguez A., Stevuelta J.L., Moreno S., Armstrong J., Forsburg S.L., A. Cruttil L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., A. Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; The genome sequence of Schizosaccharomyces pombe.";

Nature 415: 81-880 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYJ1 RAT STANDARD; PRT; 1574 AA.

GG59IO, 089092; Q629II; Q8102B;
30-WAY-2000 (Rel. 39, Last sequence update)
15-WAY-2004 (Rel. 43, Last annotation update)
Synaptojanin | EC 3.1.3.36| (Synaptic inositol-1,4,5-trisphosphate 5-phosphatase 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- FUNCTION: Component of the gamma tubule complex that is required for the regulation of both interphase microtubules and mitotic bipolar spindles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McPherson P.S., Garcia E.P., Slepnev V.I., David C., Zhang X., Grabs D., Sossin W.S., Bauerfeind R., Nemoto Y., De Camilli P., "A presynaptic inositol-5-phosphatase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Spindle pole body and the microtubule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            784 AA; 90157 MW; E529CE217FFDA2B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :|| || : |: |:|::|
592 FRYFLL---LRHVEMQLENSWVQHSKNSAWRL 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 YRYKLLINWAYQQVQQNKEDAWIEH---DVWRM 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organizing center (MTOC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Sprague-Dawley; TISSUE=Brain;
MEDLINE=96149250; PubMed=8552192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GeneDb_Spombe; SPBC365.15; -.
InterPro; IPR007559; Spc97, Spc98.
Blan; PF04130; Spc97_Spc98; 1.
Microtubule; Mitosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AL078627; CAB44767.1; -. EMBL; AB026664; BAA77269.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 31.2%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 379:353-357 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T43510; T43510.
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2

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SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
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                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00128; IPPC; 1
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1126
1545
1423
1403
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1140
1156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Multigene family.
DOMAIN 119
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CONFLICT
SEQUENCE
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DOMAIN
DOMAIN
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REPEAT
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         8
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Name=2; Synonyms=145 kDa;
IsoId=062910-2; Sequence=VSP_002686;
Name=3; Synonyms=Delta-SAC;
IsoId=062910-3; Sequence=VSP_002684;
Name=4; Synonyms=170 kDa-16AA;
IsoId=062910-5; Sequence=VSP_002685; VSP_002686;
Name=5; Synonyms=145 kDa-16AA;
IsoId=062910-6; Sequence=VSP_002684, VSP_002686;
Name=5; Synonyms=Delta-SAC-16AA;
IsoId=062910-6; Sequence=VSP_002684, VSP_002685;
IsoId=062910-6; Sequence=VSP_002684, VSP_002686;
IsoId=062910-6; Sequence=VSP_002684, VSP_002685;
IsoId=062910-6; Sequence=VSP_002685, VSP_002685;
IsoId=062910-6; Sequence=VSP_002685, VSP_002685;
IsoId=062910-6; Sequence=VSP_002685, VSP_002685;
IsoId=062910-6; Sequence=VSP_002684, VSP_002685;
IsoId=062910-6; Sequence=VSP_002685, VSP_002686;
IsoId=062910-6; Sequence=VSP_002685, VSP_002686;
IsoId=062910-6; Sequence=VSP_002685, VSP_002686;
IsoId=062910-6; Sequence=VSP_002685, VSP_002686;
IsoId=062910-6; Sequence=VSP_002685, VSP_002686,
IsoId=062910-6; Sequence=VSP_002685, VSP_002686;
IsoId=062910-6; Sequence=VSP_002685, VSP_002686,
IsoId=062910-6; Sequence=VSP_002685, VSP_002686;
IsoId=062910-6; Sequence=VSP_002685, VSP_002686,
IsoId=062910-6; Sequence=VSP_002686,
IsoId=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   compared with its expression in embryonic brain where as isoform 1 decreases to undetectable levels.

DOMAIN: Binds to EPSI5 (a clathrin coat-associated protein) via a C-terminal domain containing three Asn-Pro-Phe (NPF) repeats (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activity of synaptojanin 1.
-!- SIMILARITY: In the central section; belongs to the inositol-1,4,5-trisphosphate 5-phosphatase family.
-!- SIMILARITY: Contains 1 SAC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: 1-phosphatidy1-1D-myo-inositol 4,5-bisphosphate + H(2)0 = 1-phosphatidy1-1D-myo-inositol 4-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN: The C-terminal proline-rich region mediates binding to a variety of SH3 domain-containing proteins including AMPH, SH3GL1, SH3GL2, SH4GL3 and GRB2.

DOMAIN: Splicing of the SAC1 domain does not alter the catalytic
                                                                                                                                                                                                                                                                                                                                                                       Ringstad N., Nemoto Y., De Camilli P.,
"The SH3p4(Sh3p8/SH3p13 protein family: binding partners for
"The SH3p4(Sh3p8/SH3p13 protein family: binding partners for
"The SH3p4(Sh3p8/SH3p13) protein a Grb2-like Src homology 3 domain.";
Proc. Natl. Acad. Sci. U.S.A. 94:8569-8574(1997).
-!- FUNCTION: Inositol 5-phosphatase which has a role in clathrin-
                                                                        Woscholski R., Finan P.M., Radley E., Parker P.J.;
"Identification and characterisation of a novel splice variant of
                                                                                                                                                                                  TISSUE=Brain;
MEDLINE=96394655; PubMed=8798761;
MEDLINE=96394655; PubMed=8798761;
Mandaun A.R., McPherson P.S.;
"Tissue-specific alternative splicing generates two synaptojanin isoforms with differential membrane binding properties.";
J. Biol. Chem. 271:24856-24861(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative splicing; Named isoforms=6;
Name=1, Synonyms=170 kDa;
Name=1, Synonyms=170 kDa;
Name=1, Synonyms=170 kDa;
Name=1, Synonyms=170 kDa;
Note=A stop codon in position 1309 is suppressed due to
alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               + phosphate.
-!- SUBUNIT: Binds AMPH, SH3GL1, SH3GL2 and SH3GL3.
-!- SUBCELLULAR LOCATION: Localized mainly in the cytoplasm
                                                                                                                                                                                                                                                                                                                      INTERACTION WITH SH3GL1; SH3GL2 AND SH3GL3.
                                                       MEDLINE=98374013; PubMed=9710239;
                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97385143; PubMed=9238017
                     FROM N.A. (ISOFORM 3).
                                                                                                                                 FEBS Lett. 432:5-8(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mediated endocytosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                       ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
                                     TISSUE=Brain;
                                                                                                                  synaptojanin1
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16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Microtubule-actin crosslinking factor 1, isoforms 1/2/3 (Actin cross-
linking family protein 7) (Macrophin 1) (Trabeculin-alpha) (620 kDa
actin-binding protein) (ABP620).
MACRI OR ACF7 OR ABP620 OR KIAA0465 OR KIAA1251.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase; Alternative splicing; Repeat; Endocytosis; RNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Missing (in isoform 3 and isoform 6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Missing (In isoform 2 and isoform 5). /FTId=VSP_002686.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /FTId=VSP 002684.
Missing (in isoform 4, isoform 5 and isoform 6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G -> D (IN REF. 1; AAB60525)
G -> GG (IN REF. 2).
MISSING (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9DEESC876BAB3ADF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X 3 AA REPEATS OF N-P-F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAC.
CATALYTIC (POTENTIAL)
RNA-BINDING (RRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          002685.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5430 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 90;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        783 TYKYDLFSEDYDTSEKCRTPAWTDRVLWR 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 SYRYKLINWAYQQVQQNKEDAWIEHDVWR 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 50;
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50102; RRM, 1.
PROSITE; PS00030; RRM RNP 1; FALSE NEG.
PROSITE; PS50275; SAC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FTIG=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY-PRO.
POLY-PRO.
                                                                                                                                                                                                                                                  EMBL; AJ006855; CAA07267.1; ALT TERM.
InterPro; IPR005135; Exo endo phos.
InterPro; IPR000300; IPPC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRO-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                        Interpro; IPR000504; RNA rec mot.
Interpro; IPR002013; Syja N.
Pfam; PF03372; Exo endo phos; I.
Pfam; PF02383; Syja N; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 26.0%;
Similarity 27.6%;
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1574 AA; 172880
                                                                                                                                                                                                   EMBL; U45479; AAB60525.1;
EMBL; U91836; AAO24807.1;
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-!- SIMILARITY: Contains 37 spectrin repeats.
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HSSP; Q01082; 1BKR.
Genew; HGNC:13664; MACF1.
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SEQUENCE FROM N.A. (ISOFORM 2).
SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE=20001959; PubMed=10529403;
MEDLINE=20001959; PubMed=10529403;
Okuda T., Matsuda S., Nakatsugawa S., Ichigotani Y., Iwahashi N.,
Takahashi M., Ishigaki T., Hamaguchi M.;
Takahashi M., Ishigaki T., Hamaguchi M.;
"Molecular cloning of macrophin, a human homologue of Drosophila
kakapo with a close structural similarity to plectin and dystrophin.";
Blochem. Blophys. Res. Commun. 264:568-574(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T., "Construction of expression-ready cDNA clones for KIAA genes: manual curation of 330 KIAA clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from human brain.";
DNA Res. 4:345-349 11.947).
-!- FUNCTION: F-actin-binding protein which may play a role in cross-
linking actin to other cytoskeletal proteins. Also binds to
microtubules (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                    пd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIŜSUE=Brain;
MEDLINE=98116662; PubMed=9455484;
Seki N., Ohira M., Nagase T., Ishikawa K.-I., Miyajima N.,
Nakajima D., Nomura N., Ohara O.;
"Characterization of cDNA clones in size-fractionated cDNA libraries
                                                                                                                                                                                                                                                                                                                    "Prediction of the coding sequences of unidentified human genes. XV. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 6:337-345(1999).
                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).

BEDILINES-20026884, PubMed=10559237,
Sun Y., Zhang J., Kraeft S.-K., Auclair D., Chang M.-S., Liu Y.,
Sutherland R., Salgia R., Griffin J.D., Perland L.H., Chen L.B.;
Wholecular cloning and characterization of human trabeculin-alpha,
giant protein defining a new family of actin-binding proteins.";
J. Biol. Chem. 274:33522-33530(1999).
                                                                                                                                                                                                                                                                                     MEDLINE=20039619; PubMed=10574462;
Nagase T., Ishikawa K.-I., Kikuno R., Hirosawa M., Nomura N.,
                                                                                                                                                                                            TISSUE SPECIFICITY: Ubiquitously expressed.
SIMILARITY: Belongs to the plakin or cytolinker family.
SIMILARITY: Contains 1 actin-binding domain.
SIMILARITY: Contains 2 calponin-bomology (CH) domains.
SIMILARITY: Contains 2 EF-hand calcium-binding domains.
SIMILARITY: Contains 1 SH3 domain.
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Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=4;
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IsoId=Q9UPN3-1; Sequence=VSP_007341;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22158633; PubMed=12168954;
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SEQUENCE OF 1544-5057 FROM N.A.
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                                                                                                                                                                                                                                         Mamm. Genome 12:852-861(2001).
                                                                                                                                                                                                                                                              SEQUENCE OF 868-2350 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Res. 9:99-106(2002)
                                                                                                                                                                                                                                                                           TISSUE=Brain;
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R Probom; PD000012; E. ...
R SMART; SM0054; ERh; 2.
DR SMART; SM0054; ERh; 2.
DR SWART; SM00150; SPEC; 36.
DR PROSITE; PS00019; ACTININ 1; 1.
DR PROSITE; PS00019; ACTININ 2; FALSE_NEG.
DR PROSITE; PS50001; CH; 2.
DR PROSITE; PS500018; EF HAND; 2.
DR P
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GO; GO:0003780; F:actin cross-linking activity; NAS.
GO; GO:0005780; F:actium ion binding; NAS.
GO; GO:0008017; F:actium ion binding; NAS.
InterPro; IPRO017; F:adicrotubule binding; NAS.
InterPro; IPRO01715; Calponin-like.
InterPro; IPRO01715; Calponin-like.
InterPro; IPRO0145; EF-hand.
InterPro; IPRO0145; SH3.
InterPro; IPRO0147; Spectrin.
Pfam; PF00307; CH; 2.
Pfam; PF00307; CH; 2.
Pfam; PF00307; GAS2; 1.
Pfam; PF00185; Spectrin; 27.
Pfam; PF00185; Spectrin; 27.
Pfam; PF00187; GAS2; 1.
Pfam; PF00187; GAS2; 1.
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AB033077; BAA86565.1;
AL137853; CAC15920.1;
AB007934; BAA32310.2;
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                                                                                   Isold=Q9UPN3-3; Sequence=External;
TISSUE SPECIFICITY: Expressed in heart, lung, pituitary and
placenta, not found in brain, kidney, liver, pancreas or skeletal
                                                                                                                                                                                                                       -!- SIMILARITY: Belongs to the plakin or cytolinker family.
-!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
-!- SIMILARITY: Contains 19 plectin repeats.
-!- SIMILARITY: Contains 32 spectrin repeats.
 -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
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                  Event=Alternative splicing; Named isoforms=4;
                         Name=4;
IsoId=Q96PK2-1; Sequence=Displayed;
                                          Name=1;
IsoId=Q9UPN3-1; Sequence=External;
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IsoId=Q9UPN3-2; Sequence=External;
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SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
MEDLINE=21833812; PubMed=11845288;
Gong T.-W.L., Besirli C.G., Lomax M.I.;
MAMMI. gene structure: a hybrid of plectin and dystrophin.";
Mamm. Genome 12:852-861(2001).
--- FUNCTION: May play a role in cross-linking cytoskeletal proteins
--- by binding intermediate filaments to the N-terminal plectin
repeats and microtubules to the C-terminus.
                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                    Score 50; DB 1; Length 5430;
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10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
MACFION ACFO OR ACFO OR ARFORD ABB620 OR KIAA0465 OR KIAA1251.
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                Query Match 25.8%; Score 49.5; DB 1; Length 95; Best Local Similarity 35.5%; Pred. No. 4.5; Matches 11; Conservative 7; Mismatches 8; Indels
                                                                                                SEQUENCE FROM N.A. Okinaka R.T., Cloud K., Hampton O., Hill K.K., Keim P., La Kumano S., Manter D., Martinez Y., Svensson R., Tatum L.R. Brown A.E., Jackson P.J.; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                           Plasmid pXO2.
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                       EMBL, AF188935, AAF13609.1, -.
Hypothetical protein; Plasmid.
SEQUENCE 95 AA; 11613 MW; 2C2622DD9CFAE66F CRC64;
 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein pX02-04.
                                                                                                                                                                                                                                                                                                                                   1 RRSYRYKLLNWAY-----QOVQONKEDAWIE 26
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                                                 Bacillus anthracis.
                                                                               NCBI_TaxID=1392;
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5308 5309 SPECTRIN 30.
5316 5418 SPECTRIN 31.
5425 555 SPECTRIN 31.
5425 555 SPECTRIN 31.
5427 555 SPECTRIN 31.
5428 555 SPECTRIN 31.
5438 543 670134 MM; B8784112752DA004 CRC64;
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95 AA.

STANDARD;

RESULT 15 YQ04_BACAN ID YQ04_BACAN AC Q9RNZ8;

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Gaps

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein July 12, 2004, 14:01:53 ; Search time 17 Seconds Run on:

(without alignments)
192.383 Million cell updates/sec

US-10-010-667A-2_COPY_185_218

192 1 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI 34 Sequence:

Perfect score:

Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

PIR 78:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARIES

	Description	hypothetical prote	hypothetical prote	galactosamine-cont	ORF MSV248 probabl	hypothetical prote	hypothetical prote	hypothetical prote	phorbol ester-bind	hypothetical prote	hydantoin utilizat	hypothetical prote	hypothetical prote	`~	hypothetical prote		hypothetical prote	probable hydantoin	hypothetical prote	probable spindle p	hypothetical prote	synaptojanin, 170K	hypothetical prote		hypothetical prote	probable pathogeni	2,3,4,5-tetrahydro	hypothetical prote	ical	probable 60kda inn
SUMMAKIES	ID	B70446	\$40764	E69631	T28409	S49113	C69546	E69966	A41101	T19295	G64606	AB2102	T27222	S75895	C83260	AG2434	AG1839	G71907	AC2411	T43510	T00919	S68448	T00079	T42707	E84502	AI0697	H84956	H64458	T16602	E71537
	DB	12	7	7	N	0	7	7	~	~	7	N	0	Н	~	N	N	N	0	~	~									
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↔	ery	32.6	30.5	30.2	29.5	28.9	27.6	27.1	27.1	27.1	26.8	26.6	26.6	26.6	26.6	26.3	26.3	26.3	26.0	26.0	26.0	26.0	26.0	26.0	25.8	25.8	25.8	25.8	25.8	25.8
	Score	i N	58.5	58	56	55.5	53	52	52	52	51.5	51	51	51	51	50.5	50.5	50.5	20	50	20	20	20	50	49.5	O1	U١	49.5	49.5	49.5
	Result No.	! ! H !	7	ო	4	5	9	7	∞	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

alyl tRNA syntheta valine-tRNA ligase	hypothetical prote protein F09C3.1 [i	tRNA pseudouridine hypothetical prote	hypothetical prote	hypothetical prote	glycerol kinase [i	protein F54D8.1 [i	RNA-directed RNA p	translation initia	hypothetical prote	hypothetical prote	conserved hypothet	hypothetical prote
F86502 B72120	T20642 E87998	A82691	H84700	T40609	AE2032	HB8449	T00133	C90257	T04751	T33477	B81021	T20944
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49.5	49.5	4 4	4.9	49	49	49	49	48.5	48.5	48.5	48.5	48.5

ALIGNMENTS

RESULT 1

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hypothetical protein ad_1687 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: OB.May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: B70446
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham,
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D.E.; 9

Nature 392, 353-358, 1998 A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Accession: B70446

A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-480 <AQP> A;Residues: 1-480 <AQP> A;Cross-references: GB:AE000751; NID:g2984013; PIDN:AAC07560.1; PID:g2984016; GB:AE00068 A;Experimental source: strain VF5 C;Genetics:

A;Gene: aq_1687

Gaps 15; Length 480; Indels Query Match 32.6%; Score 62.5; DB 2; Best Local Similarity 25.0%; Pred. No. 1.8; Matches 12; Conservative 17; Mismatches 4;

2

1 RRSYR-----YKLLNWAYQ--QVQQNKEDAWIEHDVWRME 33 57 10 RKTYRLKIPAKVSIDGKEYKVLDWSYEGFRIEKSKEDVFEKDKVYKVK g ð

hypothetical protein ZK512.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 24-Nov-1999 A;Reference number: \$40759
A;Accession: 840764
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1418 <HAW>
A;Cross-references: EMBL: 222177; NID: 9297989; PID: 9297992
C;Genetics: C;Accession: S40764 R;Hawkins, T.; Ainscough, R. submitted to the EMBL Data Library, February 1993

772/3; 846/3; 946/1; A,Introns: 199/1; 238/1; 290/2; 529/3; 557/3; 588/3; 677/2; 733/3; C;Superfamily: Caenorhabditis elegans hypothetical protein ZK512.3

Gaps 3; DB 2; Length 1418; Indels Query Match
30.5%; Score 58.5; Di
Best Local Similarity 43.5%; Pred. No. 19;
Matches 10; Conservative 5; Mismatches

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15 QVQQNKED---AWIEHDVWRMEI 34

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Cypace: Orlean 1990 #Sequence_revision 12-may-1995 #text_cnange 23-mar-2001

RyJuerchott, K.; Boerner, T.

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RyJuerchott, K.; Boerner, T.

RyJuerchott, K.; Boerner, T.

RyDescription: Sequence of the cyanobacterial plasmid pMA1 from Microcystis aeruginosa A; Reference number: 849112

A; Reference number: 849113

A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein AF2371 - Archaeoglobus fulgidus
CiSpecies: CoS-Dec-1997 #text_change 22-Oct-1999
CiAccession: C69546
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.B.; Ketchum, K.A.; Dodso
i; Pleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.P.; McDonald, L.
Nature 390, 364-370, 1997
A.Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S
Smith, H.O.; Woese, C.R.; Venter, J.C.
A.Tile: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae
A.Reference number: A69250; MulD:98049343; PMID:9389475
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
A.Residues: 1-152 <KLE>
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C;Species: Bacillus subtilis
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C;Species: Bacillus subtilis
C;Date: OS-Dec-1997 #sequence_revision OS-Dec-1997 #text_change 15-Oct-1999
C;Accession: E69966
R;Kunst, F:; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; CA.; Bruitch, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Febret, C.; Ferrari, E.
A;Authors: Foulgar, D.; Fritz, C.; Fullta, M.; Fulita, Y.; Funs, S.; Galle, A.; Honaut, A.; Hilbert, M.; Kurita, K.; Lapidus, A.; Galle
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee
A;Authors: Schlach, A.; Oddega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Porathol
A;Authors: Schlach, A.; Tanaka, E.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serohon
A;Authors: Schlach, A.; Tanaka, T.; Terpstran, P.; Tognoni, J.; Sekowska, A.; Serohon
A;Authors: P.; Wipat, A.; Tanaka, T.; Terpstran, P.; Tognoni, A.; Tosato, V.; Vochiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yasumoto, K.; Yasumoto, K.; Yasumoto, K.; Yasumoto, K.; Yasumoto, K.; Yasumotos: Yoshikawa, H.; Danchin, A.; Tanaka, H.; Danchin, A.; Tognoni, A.; Danchin, A.; Tognoni, 
                                                          C'Species: Microcystis aeruginosa
C'Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-502 <JUE>
A;Cross-references: EMBL:Z28337; NID:g509352; PIDN:CAA82191.1; PID:g509354
C;Superfamily: Microcystis aeruginosa hypothetical protein 2
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Pred. No. 16;
7; Mismatches 14; Indels 19
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                     hypothetical protein 2 - Microcystis aeruginosa
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21 RYKLLSWLVRDYERNRVGAYI 41
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                                                                                                                                                                                                                                                                                Glactosamine-containing minor teichoic acid biosynthesis ggaB - Bacillus subtilis
CiSpecies: Bacillus Sistemation OS-Dec-1997 #text_change 15-Oct-1999
CiSpecies: Bacillus Sistemation OS-Dec-1997 #text_change 15-Oct-1999
CiSpecies: Bacosilier, Si, Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chans, S.; Enrilot, S.D.; Emrinch, S.D.; Emrinch, S.D.; Emrinch, S.D.; Emrinch, S.D.; Emrinch, S.; Fumano, J.; Fuma, S.; Galizzi, A.; Galler Arbuthors: Founder, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iseth, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Kongh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarvoic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y.; M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parko, V.; Pohl, T.H.; Parko, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Sadole, Y.; Sato, T.; Scanlon, A; Authors: Schletch, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serok, A; Authors: Yoshikawa, H.; Danchin, A.; Tamakoshi, A.; Tamaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, M.; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A; Richers Positkawa, H.F.; Zumstein, B.; Yoshikawa, H.; Danchin, A.; A; Pater, M.; A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-900 cKUN>
A;Residues: 1-900 cKUN>
A;Rorss-references: GB:Z99122; GB:AL009126; NID:g2636029; PIDN:CAB15585.1; PID:e1184474;
A;Experimental source: strain 168
C;Genetics:
A;Gene: ggaB
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C;Species: Melanoplus sanguinipes entomopoxvirus
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
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A;Molecule type: DNA
A;Residues: 1-150 <AFO>
A;Coss-references: EMBL:AF063866; NID:g4049647; PIDN:AAC97724.1; PID:g4049764
C;Genetics:
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R;Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
Tyrol. 73, 533-552, 1999
A;Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A;Reference number: Z20484; MUID:99102612; PMID:9847359
A;Accession: T28409
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41.7%; Pred. No. 3.8;
iive 1; Mismatches 7; Indels
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: | : | : | | | | | | | : : 1355 EVAENENDIDNAWTEHDVWAISL 1377
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Matches 10; Conservative
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Riromb, J.T.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenneson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Natuke 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A;Reference number: A64520; MUID:97394467; PMID:9252185
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An. A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 1
A;Introns: 25/1; 35/1; 68/2; 105/2; 149/1; 170/3; 186/1; 235/3; 412/2; 434/2; 500/2; 540
1748/1; 1781/3
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A;Cross-references: GB:AE000582; GB:AE000511; NID:g2313812; PIDN:AAD07746.1; PID:g231382
C;Superfamily: Pseudomonas D-amino acid hydantoin hydrolase (ATP-hydrolyzing) hyuA
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C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
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A,Molecule type: DNA
A;Residues: 1-90 «KUR»
A;Cross-references: GB:BA000019; PIDN:BAB74068.1; PID:g17131461; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                     A;Accession: T27889
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1813 (WI3>
A;Cross-references: EMBL:Z73912; PIDN:CAA98147.1; GSPDB:GN00019; CESP:ZK524.2a
A;Experimental source: clone ZK524
A;Genetics:
A;Genetics:
A;Genetics:
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C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 16-Feb-2001
C;Accession: G54606
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653 RKFYRHK-------KWVDADVWQME 670
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5; Mismatches
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          submitted to the EMBL Data Library, June 1996
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Matches 10; Conservative
                                                                     A; Reference number: Z20435
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A,Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A,Reference number: A69580; MUD:98044033; PMID:9384377
A,Accession: B69966
A,Status: preliminary, nucleic acid sequence not shown; translation not shown A,Residues: 1-79 < KUN>
A,Residues: 1-79 < KUN>
A,Cross-references: GB:299116; GB:AL009126; NID:g2634723; PIDN:CAB14297.1; PID:e1185634; C,Genetics: A,Gene: yqkC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phorbol ester-binding protein unc-13 - Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Species: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 23-Feb-1997
C;Accession: A41101
R;Maruyana, I.N.; Brenner, S.
R;Maruyana, I.N.; Brenner, S.
Proc. Natl. Acad. Sci. U.S.A. 88, 5729-5733, 1991
A;Title: A phorbol ester/diacylglycerol-binding protein encoded by the unc-13 gene of (A;Reference number: A41101;MUID:91288538; PMID:2062851
A;Accession: A41101
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R;Lloyd, C.
submitted to the EMBL Data Library, March 1997

A,Reference number: Z19198

A,Accession: T19931

A,Status: preliminary; translated from GB/EWBL/DDBJ

A,Residues: 1-1813 < MI2>
A,Residues: 1-1813 < MI2>
A,Residues: 1-1813 < MI2>
A,Residues: creferences: EMBL:Z92779; PIDN:CAB07173.1; GSPDB:GN00019; CESP:ZK524.2a
A,Bardner, A.
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A;Molecule type: DNA
A;Residues: 1-1813 <WIL>
A;Cross-references: EMBL:Z79694; PIDN:CAB01966.1; GSPDB:GN00019; CESP:ZK524.2a
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Cyspecies: Ti-Oct-1999 #sequence revision 15-Oct-1999 #text_change 02-Sep-2000
Cyspecies: Ti-Oct-1999 #sequence revision 15-Oct-1999 #text_change 02-Sep-2000
Cyspecies: Ti-Oct-1999 #sequence revision Intervention Intervent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 27.1%; Score 52; DB 2; Length 79; Best Local Similarity 28.1%; Pred. No. 6.4; Matches 9; Conservative 8; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 RSYRYKLLNWAYQQVQQNKEDAWIEHDVWRME 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     430 NWRYDSIQEEDNEKDNWKQH 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 NWAYQQVQQ--NKEDAWIEH 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
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completed: July 12, 2004, 14:11:19
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les 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 26.6
Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Matches
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Job time
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable L-xylulokinase (EC 2.7.1.53) - Synechocystis sp. (strain PCC 6803)
G.Species: Synechocystis sp.
A.Varietr, PCC 6803
G.Date: 10-Sep-1999 #text_change 16-Jun-2000
G.Accession: S75895
F.Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA, Res. 3, 109-136, 1996
A.; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Molecule: 1-495 «KMN»
A;Cross-references: EMBL:D90913; GB:AB001339; NID:g1653348; PIDN:BAA18354.1; PID:g165344
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: xylulokinase
C;Keywords: phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                Rimcourzay, A.

Submitted to the EMBL Data Library, September 1997

A.Reference number: 220330

A.Reference number: 220330

A.Status: preliminary; translated from GB/EMBL/DDBJ

A.Molecule type: DNA

A.Molecule type: DNA

A.Residues: 1-44 /WILA

A.Cross-references: EMBJ:292281; PIDN:CAB16511.1; GSPDB:GN00022; CESP:Y57G11C.10

A.Experimental source: clone Y57G11C

C.Genetics:
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                                                                                                                                                                                                                                                                                            hypothetical protein Y57G11C.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 26-May-2000
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 54;
4; Mismatches 7; Indels
                                                  DB 2; Length 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 495;
                                                                                               7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: S74322; MUID:97061201; PMID:8905231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Map position: 4
A;Inkrons: 332/1; 416/3
C;Superfamily: human GDP dissociation inhibitor XAP-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 YEGNIVGQAYKELTQFYPKAGWVEHDALEIWR 57
                                        Query Match
26.6%; Score 51, DB 2
Best Local Similarity 46.2%; Pred. No. 9.9;
Matches 12; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 51; DB 1
Pred. No. 60;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 YRYKLLNWAYQQVQQNKEDA-WIEHD---VWR 31
                                                                                                                                                                       24 LNWNYQOFKDCFSFKVNNEAIEIEHD 49
                                                                                                                                      9 INWAYQOVQO-----NKEDAWIEHD 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138 KRRFK-KFLVWV-QQFDENKEDTW 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RRSYRYKLLNWAYQQVQQNKEDAW 24
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Best Local Similarity 34.4%;
Matches 11; Conservative 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 26.6%;
Best Local Similarity 45.8%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                    Accession: T27222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S75895
A; Gene: asr2369
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RESULT 14

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Cispecies: Pseudomonas acrossing integrated in Sequence in Section Section (Signature Fact) (Signature Inc.) (Signature Inc.)
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R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch
R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch
R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch
DNA Res. 8, 205-213, 2001
A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
A; Reference number: AB1807; MUD:21595285; PMID:11759840
A; Accession: AG2434
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-201 <KUR>
A; Residues: 1-201 <KUR>
A; Residues: 1-201 <KUR>
A; Cross-references: GB:BA000019; PIDN:BAB76730.1; PID:g17134169; GSPDB:GN00179
C; Genetics: C; Genetics: Strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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hypothetical protein PA3079 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein alr5031 [imported] - Nostoc sp. (strain PCC 7120) C; Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7; C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 793;
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C;Superfamily: Synechocystis hypothetical protein slr2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.6%; Score 51; DB 2; 52.9%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
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401 VQRSKDDAVREHPFWRL 417
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(without alignments)
176.480 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US07_NEW PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US07_NEW PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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13: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
                                                                                                                                                                                         July 12, 2004, 14:10:33 ; Search time 60.093 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                   1 RRSYRYKLINWAYQQVQQNKEDAWIEHDVWRMEI 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1279676 seqs, 311918243 residues
                                                                                                                                                                                                                                                                                                                        US-10-010-667A-2_COPY_185_218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                           - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                           OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database:
                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                             Run on:
                                                                                                                                                                                                                                                                                                                            Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Sequence 50, Appl
Sequence 51, Appl
Sequence 51, Appl
Sequence 51, Appl
Sequence 879, App
Sequence 27, Appl
Sequence 2, Appl
                                                      Sequence 20, Appl
Sequence 20, Appl
Sequence 38, Appl
                                 Description
                                                                                  US-09-747-835A-50
US-09-747-835A-51
US-09-747-835A-51
US-10-312-312-50
US-09-759-143-879
US-09-759-143-879
US-09-822-827-879
US-09-822-827-879
US-09-895-793-879
US-09-895-793-879
US-09-895-793-879
US-09-895-793-879
US-09-895-793-879
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US-09-895-793-879
US-09-895-793-879
US-10-205-267-13
                                                    US-10-011-095-20
US-10-010-667A-20
US-10-165-044-38
SUMMARIES
                                                                                      991199
                                Match Length DB
                                                                                                                                                                                       100.0
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                                                              Score
                    Result
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Sequence 879, App	Sequence 2, Appli	9	87	87	37	71,	13	72.	2	O		ω	æ	Sequence 15, Appl	Sequence 15, Appl	Н	æ	Н	Н	Н	32,	88	89	90	91,	92	10,	Sequence 3, Appli
US-10-012-896-879	US-10-010-667A-2	US-10-205-823-397	US-10-144-678A-879	US-10-294-025-879	ᅼ	US-10-295-027-714	US-10-295-027-1347	US-10-425-114-72779	US-10-165-044-2	US-10-455-822-93	US-09-963-896-1	US-10-011-095-8	US-10-010-667A-8	US-09-747-835A-15	US-10-312-312-15	US-10-455-822-11	US-10-455-822-80	US-10-455-822-172	0	0	US-10-239-607-32	US-10-455-822-88	US-10-455-822-89	US-10-455-822-90	2	US-10-455-822-92	US-09-888-257A-10	US-10-455-822-3
13	14	14	14	74	15	15	15	12	14	12	6	14	14	σ	12	12	12	12	12	12	15	12	12	12	12	12	10	12
339	339	339	339	339	339	339	339	368	375	443	141	173	173	237	237	419	419	419	419	419	419	444	444	444	444	444	454	454
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	57.3	55.7	55.7	55.7	55.7	55.7	55.7	55.7	55.7	55.7	55.7	55.7	55.7	55.7	55.7	55.7	55.7	55.7	55.7
192	192	192	192	192	192	192	192	192	192	110	107	107	107	107	107	107	107	107	107	107	107	107	107	107	107	107	107	107
16	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Sequence 20, Application US/10011095
; Beduence 20, Application US/10011095
; Publication No. US20030045682A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
APPLICANT: Raitano, Arthur B.
; APPLICANT: Raitano, Douglas C.
; APPLICANT: Saffran, Douglas C.
; APPLICANT: Mitchell, Steve Chappell
; TITLE OF INVENTION: ANTHEODIES IMMUNOSPECIFIC FOR STEAPI (AS AMENDED)
; FILE REFERENCE: 51158200161, 205
; CURRENT APPLICATION NUMBER: 05/10/11,095
; CURRENT APPLICATION NUMBER: 06/091,183
; PRIOR APPLICATION NUMBER: 60/091,183
; PRIOR PILING DATE: 1999-06-01
; PRIOR PILING DATE: 1999-06-30
; RIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 34
; TYPE: PRI
; ORGANISM: Artificial Sequence
; FRATURE:
; OTHER INFORMATION: STEAP-1 peptide
; OCHER INFORMATION: STEAP-1 peptide
; Marches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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1 RRSYRYKLIAWAYQQVQQNKEDAWIEHDVWRMEI 34

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CURRENT FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: US 09/729,739
PRIOR FILING DATE: 2000-12-04
PRIOR FILING DATE: 2000-12-04
PRIOR FILING DATE: 2000-08-31
PRIOR FILING DATE: 2000-08-31
PRIOR FILING DATE: 2000-08-31
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38
LENGTH: 34
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Patent No. US20020146692A1
GENERAL INFORMATION:
APPLICANT: Yamazaki, Victoria
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 50, Application US/09747835A Patent No. US20020146692A1
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SEQ ID NO 50
LENGTH: 267
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GENERAL INFORMATION:
APPLICANT: YamazaKi, Victoria
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Liu, Chenghua
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Wang, Dunrui
                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-165-044-38
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US-09-747-835A-50
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US-09-747-835A-51
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APPLICANT: Aya Jakobovits
TITLE OF INVENTION: ROYEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 51158-2016.02
CURRENT APPLICATION NUMBER: US/10/165,044
CURRENT APPLICATION NUMBER: US 60/087,520
PRIOR APPLICATION NUMBER: US 60/081,183
PRIOR FILING DATE: 1998-06-01
PRIOR PRILING DATE: 1998-06-30
PRIOR PRILING DATE: 1999-06-30
PRIOR PLING DATE: 1999-06-01
PRIOR PRILING DATE: 1999-06-01
PRIOR PILING DATE: 1999-06-01
PRIOR PILING DATE: 1999-06-01
PRIOR PILING DATE: P999-06-01
PRIOR PILING DATE: P999-06-01
PRIOR PILING DATE: P999-06-01
PRIOR PILING DATE: POTO-06-01
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APPLICANT: Saffran, Douglas C.
APPLICANT: Saffran, Douglas C.
APPLICANT: Saffran, Douglas C.
TITLE OF INVENTION: STEPERTINE TRANSMEMBRAME ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILES REFERENCE: 511582001601
CURRENT APPLICATION NUMBER: US/10/10,667A
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR PRILING DATE: 1999-06-01
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOFTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 34
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                                                                                                  Sequence 20, Application US/10010667A Publication No. US20030055217A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Daniel B.H. Afar
Steven Chappell Mitchell
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Publication No. US20030149531A1
GENERAL INFORMATION:
APPLICANT: Agensys, Inc.,
APPLICANT: Rene S. Hubert
APPLICANT: Arthur B. Raitano
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas Saffran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: STEAP-1 peptide US-10-010-667A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                     APPLICANT: Afar, Daniel
APPLICANT: Hubert, Rene S.
APPLICANT: Leong, Kahan
                                                                               US-10-010-667A-20
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US-10-165-044-38
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APPLICANT:
APPLICANT:
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APPLICANT: Zhang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Ren, Feiyan
APPLICANT: Dramanac, Nadoje T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIK
TITLE OF INVENTION: LIKE) POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: HYS-37CIP
CURRENT APPLICATION NUMBER: US/09/747,835A
CURRENT FILING DATE: 2002-03.08
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Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e-18;
Matches 34; Conservative 0; Mismatches 0;
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100.0%; Score 192; DB 9;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 34; Conservative 0; Mismatches 0;
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                                                                                                      1 RRSYRYKLINWAYQQVQQNKEDAWIEHDVWRMEI 34
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APPLICANI: ASIMILA, MINICANII ARABILALS, RELATING TO G PROTEIN-COUPLED RECEPTOR-LIKE TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIKE FILE OF INVENTION: LIKE) POLYBEPTIDES AND POLYNUCLECTIDES CURRENT APPLICATION NUMBER: US/10/312,312
CURRENT APPLICATION NUMBER: US/10/312,312
CURRENT APPLICATION NUMBER: US 09/729,739
PRIOR PILING DATE: 2000-12-04
PRIOR PILING DATE: 2000-12-04
PRIOR PILING DATE: 2000-08-31
PRIOR PILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US 09/620,312
PRIOR APPLICATION NUMBER: US 09/520,317
PRIOR APPLICATION NUMBER: US 09/520,317
PRIOR PILING DATE: 2000-04-25
PRIOR PILING DATE: 2000-04-25
PRIOR PILING DATE: 2000-04-25
PRIOR PILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PATENTING NOS: 63
SEQ ID NOS: 63
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100.0%; Pred. No. 1.6e-17;
Live 0; Mismatches 0;
                                                                                                                                             Query Match 100.0%; Score 192; DB 12;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 34; Conservative 0; Mismatches 0;
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Patent No. US2002022248A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                       Sequence 51, Application US/10312312 Publication No. US20040068097A1 GENERAL INFORMATION:
; SOFTWARE: Patentin version 3.0; SEQ ID NO 50; EBNGTH: 267; TYPE: PRT; TYPE: PRT CRANIEN: HOMO Sapiens US-10-312-312-50
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hyseq, Inc.
APPLICANT: Yamazaki, Victoria
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
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Best Local Similarity 100.0
Matches 34; Conservative
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Wang, Dunrui
Zhang, Jie
Ren, Feiyan
Asundi, Vinod
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US-09-759-143-879
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APPLICANT: Ren, Felyan
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: Branac, Radoje T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIKE
TITLE OF INVENTION: LIKE) POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: LIKE) POLYPEPTIDES AND FOLYNUCLEOTIDES
CURRENT APPLICATION NUMBER: US/09/747,835A
CURRENT FILLING DATE: 2002-03-08
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100.0%; Score 192; DB 9;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 34; Conservative 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: US 09/729,739
PRIOR APPLICATION NUMBER: US 09/729,739
PRIOR APPLICATION NUMBER: US 09/653,450
PRIOR FILING DATE: 2000-08-31
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US 09/598,042
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
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FILING DATE: 2000-01-21
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SOFTWARE: Patentin version 3.0
SEQ ID NO 51
LENGTH: 267
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DB 9; Length 339;

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Query Match
100.0%; Score 192; DB 9;
Best Local Similarity 100.0%; Pred. No. 2e-17;
Matches 34; Conservative 0; Mismatches 0;
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; ORGANISM: Homo sapiens
US-09-822-827-879
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ORGANISM: Homo sapiens
                                                                                                                                                                         RESULT 10
US-09-822-827-879
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US-09-802-520-11
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 21012.427023
FULE REFERENCE: 21012.427023
CURRENT APPLICATION NUMBER: US/09/759,143
NUMBER OF SEQ ID NOS: 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGOSIS OF PROSTATE CANCER
FILE REFERENCE: 210.11.427024
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
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100.0%; Pred. No. 2e-17;
Live 0; Mismatches 0; Indels
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FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 879, Application US/09780669 Patent No. US20020051977A1 GENERAL INFORMATION:
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
                 Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
                                                                 Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samel
Harlocker, Susan L.
                                                                                                                                                                                      Wang, Aijun
Skeiky, Yasir A.W.
Hepler, William
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Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
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Skeiky, Yasir A.W.
Hepler, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-143-879
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US-09-780-669-879
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                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 879
              APPLICANT:
APPLICANT
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APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                      Sequence 879, Application US/09822827

Batent No. US20020081680A1

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSIATE CANCER
FILE REFERENCE: 210.11.534C1
CURRENT APPLICATION NUMBER: US/09/822,827

CURRENT FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 982

SOFTWARE: FastSEQ for Windows Version 3.0
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100.0%; Score 192; DB 9; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-17;
Matches 34; Conservative 0; Mismatches 0; Indels (
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; OTHER INFORMATION: Incyte ID No. US20020187472A1 g6572948
US-09-802-520-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 192; DB 9;
Best Local Similarity 100.0%; Pred. No. 2e-17;
Matches 34; Conservative 0; Mismatches 0;
                                                                                 185 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI 218
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Publication No. US20020187472A1
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Chen, Huel-Mei
APPLICANT: Ison, Craig H.
ITLE OF INVENTION: STEAR-RELATED PROTEIN
FILE REFERENCE: PC-0037 US
CURRENT FAILNG DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 11
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US-09-895-793-879

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Sequence 2, Application US/10408009; Publication No. US20040072196A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                             34; Conservative
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CRGANISM: Homo sapiens
US-09-895-814-879
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Best Local Similarity
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US-10-408-009-2
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APPLICANT: Foy, Teresa
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FRASESQ for Mindows Version 3.0
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Houghton, Raymond L.
Vinals de Bassols, Carlota
Foy, Teresa
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Vinals de Bassols, Carlota
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Sequence 879, Application US/09895793
Publication No. US20020192763A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C. APPLICANT: Mitcham, Jennifer L. APPLICANT: Harlocker, Susan L. APPLICANT: Jiang, Yuqiu APPLICANT: Kalos, Michael D.
                                                                                                                                                                                                                                                                                              Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
Hural, John
                                                     APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Micham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yoqiu
APPLICANT: Kalos, Michael D.
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Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
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Skeiky, Yasir A.W.
Hepler, William T.
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Best Local Similarity 100.
Matches 34; Conservative
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US-09-895-793-879
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LENGTH: 339
TYPE: PRT
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APPLICANT:
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RESULT 14

US-10-205-267-13

US-10-205-267-13

i Sequencial No. US20030064397A1

j Publication No. US20030064397A1

j GENERAL INFORMATION:

j APPLICANT: Spancake, Kimberly M.

j APPLICANT: Each and K.

j APPLICANT: Lal, Preeti G.

j APPLICANT: Lal, Preeti G.

j TITLE OF INVENTION: TRANSWEMBRANE PROTEIN DIFFERENTIALLY EXPRESSED IN PROSTATE AND LI.

j TITLE OF INVENTION: TRANSWEMBRANE US/10/205,267

j CURRENT APPLICATION UNDER: US/10/205,267

j CURRENT PILING DAIE: 2002-07-24

j SOFTWARE: PERL PROGRAM

j SEQ ID NO: 13

j ENDIFFERENT: 339
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APPLICANT: Rene S. Hubert
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Stephen C. Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
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APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C26
CURRENY APPLICATION NUMBER: US/09/895,814
CURRENY FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SSGTWARE FASSEQ for Windows Version 3.0
SGTWARE: FastSEQ for Windows Version 3.0
LENGTH: 339
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DATABASE ACCESSION NUMBER: Genbank ID No: 96572948
US-10-205-267-13
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Best Local Similarity 100.0%; Pred. No. 2e-17;
Matches 34; Conservative 0; Mismatches (
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CURRENT APPLICATION NUMBER: US/10/408,009
CURRENT FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 09/455,486
PRIOR FILING DATE: 1999-12-06
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### PRIOR APPLICATION NUMBER: 09/323,873
| PRIOR FLING DATE: 1999-06-01
| NUMBER OF SEQ ID NOS: 36
| SOFTWARE: FastSEQ for Windows Version 4.0
| LANGTH: 339
| TYPE: BRT
| ORGANISM: Homo sapiens
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; Sequence 2, Application US/09323873A
; Patent No. 6329503
; GENERAL INFORMATION:
; APPLICANT: Daniel B. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Rahan Leong
; APPLICANT: Arthur B. Raitano
; APPLICANT: Steve Chappell Mitchell
RESULT 1
US-09-323-873A-20
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US-09-323-873A-2
TYPE: PRT
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63, Appl
2, Appli
26357, A
12436, A
2607, Ap
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5163, Ap
7850, Ap
4565, Ap
28767, A
436, App
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10, Appl
10, Appl
5472, Ap
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1, Appli
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2, Appli
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Sequence 2, Appli
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                                                                                                                  July 12, 2004, 14:04:08 ; Search time 20.9535 Seconds
(without alignments)
83.770 Million cell updates/sec
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PoTUS_COMB.pep:*
                    GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-323-873A-2

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US-09-323-873A-8

US-09-323-873A-3

US-09-543-681A-5163

US-09-543-681A-7850

US-09-543-681A-7850

US-09-543-681A-7850

US-09-198-452A-111

US-09-198-452A-111

US-09-108-452A-111

US-09-205-288-64

US-09-205-288-64

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US-09-108-40-10

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1 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI 34
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US-09-600-087-2
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US-09-489-039A-12436
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB
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Sequence 13050, A
Sequence 26916, A
Sequence 7358, Ap
Sequence 4173, Ap
Sequence 20980, A
Sequence 20980, A
Sequence 27, Appl
Sequence 2, Appli
                                                                                                                                                                                                                                                                       Sequence 9477, Ap
Sequence 67, Appl
Sequence 6640, Ap
Sequence 9385, Ap
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| Sequence 20, Application US/09323873A
| Patent No. 6329503
| Patent INCORMITON:
| APPLICANT: Daniel E. Afar
| APPLICANT: Rene S. Hubert
| APPLICANT: Rene S. Hubert
| APPLICANT: Arthur B. Raitano
| APPLICANT: BY SEVENCHION: EXPRESSED IN HUMAN CANCERS AND USES THERBOF
| TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THERBOF
| TITLE OF INVENTION: BY SERVENTION: BY SERVENTION NUMBER: 00/09/323,873A
| CURRENT APPLICATION NUMBER: 00/091,183
| PRIOR FILING DATE: 1998-06-01
| PRIOR FILING DATE: 1998-06-30
| NUMBER OF SEQ ID NOS: 32
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 20
| LENGTH: 34
                    Sequence
                                                           Sequence
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                                                                       US-09-198-452A-19
US-09-198-452A-19
US-09-489-033A-13050
US-09-328-352-7358
US-09-107-532A-4173
US-09-252-991A-20980
US-09-26-551-17
US-09-489-033A-9395
US-09-489-033A-9477
US-09-198-452A-67
US-09-198-452A-67
US-09-107-532A-6640
US-09-489-033A-6440
US-09-107-532A-5449
US-09-121-979-4
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US-09-239-867-2
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100.0%; Score 192; DB 4;
Best Local Similarity 100.0%; Pred. No. 5.5e-20;
Matches 34; Conservative 0; Mismatches 0;
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TITLE OF INVENTION: MOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 129.16USU2
CURRENT APPLICATION NUMBER: US/09/323,873A
CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR PILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR PILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 339
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION UNMERS: US/09/685,166A
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SUFTWARE: FastSEQ for Windows Version 3.0
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100.0%; Score 192; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 7.2e-19;
Matches 34; Conservative 0; Mismatches 0; Indels
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100.0%; Score 192; DB 4;
Best Local Similarity 100.0%; Pred. No. 7.2e-19;
Matches 34; Conservative 0; Mismatches 0;
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Patent No. 6630305
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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Henderson, Robert A.
Kalos, Michael D.
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Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
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Retter, Marc W.
Stolk, John A.
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US-09-323-873A-2
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; Sequence 1, Application US/09083521

US-09-083-521-1

RESULT 4

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Gaps
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APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Reane S. Hubert
APPLICANT: Reane S. Hubert
APPLICANT: Arthur B. Raitano
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: BERPESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 129.16USU2
CURRENT APPLICATION NUMBER: 60/091,230
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Calegler, Karl J.
APPLICANT: Corley, Neil C.
TILLE OF INVENTION: PROSTATE GROWTH-ASSOCIATED MEMBRANE PROTEINS
NUMBER OF SEQUENCES: 7
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                                                                                                                                                                                                                                                ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPACIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
US/09/083,521
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                                                                                                    ADDRESSER: LINCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/09323873A
Patent No. 6329503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGIEVRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 58.8
Matches 20; Conservative
                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHI
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; CLONE: 1691243
US-09-083-521-1
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APPLICANT: GARY ERETON
TITLE OF INVENTION: DIGGREGATICS ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-328-352-4565

Sequence 4565, Application US/09328352

Sequence 4565, Application US/09328352

Sequence 4565, Application US/09328352

Sequence 4565, Application US/09328352

GENERAL INFORMATION: Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: NUMBER: US/09/328,352

TITLE OF TITLE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 4565

LENGTH: 166
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Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AEROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
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  Indels
  8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.1%; Score 52; DB 4 ilarity 27.6%; Pred. No. 7.5; Conservative 7; Mismatches
                                                                   8; Mismatches
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Mismatches
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                                                                                                                                                                                 Sequence 7850, Application US/09543681A
Patent No. 6605709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Acinetobacter baumannii
US-09-328-352-4565
  5.
                                           6 YKLLN-WAYQQVQQNKED----
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Best Local Similarity 30.3%;
Matches 10; Conservative
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  12; Conservative
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Best Local Similarity
Matches 8; Conserv
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    Matches
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Sequence 5163, Application US/09543681A

Patent No. 6605709

GENERAL INFORMATION:
APPLICANT: GARY BRETON

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 5163

LENGTH: 320
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APPLICANT: Arthur B. Raitano
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/323,873A
CURRENT FILING DATE: 1999-06-01
PRIOR PILLING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-01
SPRIOR FILING DATE: 1998-06-01
SPRIOR FILING DATE: 1998-06-01
SPRIOR FILING DATE: 1998-06-01
SPRIOR FILING DATE: ROSE ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                      1 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI 34
                                                                                                                                                       5; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                        Sequence 32, Application US/09323873A
Patent No. 6329503
GENERAL INFORMATION:
APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.3%; Scillarity 100.0%; P. Conservative 0;
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58.8%;
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ORGANISM: Proteus mirabilis
                                                                                                                                                       20; Conservative
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      LENGTH: 173
TYPE: PRT
ORGANISM: Homo Sapiens
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Best Local Similarity
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Best Local Similarity
Matches 15; Conserv
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Best Local Similarity
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US-09-323-873A-32
                                                    ; ORGANISM: Hor
US-09-323-873A-8
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APPLICANT:
APPLICANT:
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APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins FILE REFERENCE: PZOO2P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT PILING DATE: 1998-09-08
BARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
CURRENT FILING DATE: 1999-02-18
PPTOR APPLICATION NUMBER: US 60/074,788
                     PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 789
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R APPLICATION NUMBER: 60/047,615

RR FILING DATE: 1997-05-23

RAPPLICATION NUMBER: 60/047,597

RR FILING DATE: 1997-05-23

RR APPLICATION NUMBER: 60/047,502

RR FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/046,333
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/040,626
FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,334
FILING DATE: 1997-03-07
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EARLIER APPLICATION NUMBER: 60/040,336
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APPLICATION NUMBER: 60/047,600
FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,618
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,592
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APPLICATION NUMBER: 60/047,581
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APPLICATION NUMBER: 60/047,500
FILING DATE: 1997-05-23
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                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-09-149-476-436
'Sequence 436, Application US/09149476
'Patent No. 6420526
                                                                                                                                      TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                     397 VQRSKDDAVREHPFWRL 413
                                                                                                                                                                                                                                                                 16 VOONKEDAWIEHDVWRM 32
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R FILING DATE: 1997-05-23

RR APPLICATION NUMBER: 60/047,492

RR FILING DATE: 1997-05-23

RR APPLICATION NUMBER: 60/047,598

RR FILING DATE: 1997-05-23

RR APPLICATION NUMBER: 60/047,613

RR APPLICATION NUMBER: 60/047,582

RR APPLICATION NUMBER: 60/047,595

RR PILING DATE: 1997-05-23

RR APPLICATION NUMBER: 60/047,596

RR FILING DATE: 1997-05-23

RR APPLICATION NUMBER: 60/047,612

RR FILING DATE: 1997-05-23

RR FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/043,314
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,569
                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/047,632
FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,580
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APPLICATION NUMBER: 60/043,311
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APPLICATION NUMBER: 60/043,671
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APPLICATION NUMBER: 60/043,674
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FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,312
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APPLICATION NUMBER: 60/043,672
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APPLICATION NUMBER: 60/043,315
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APPLICATION NUMBER: 60/056,886
FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,878
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APPLICATION NUMBER: 60/043,313
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APPLICATION NUMBER: 60/048,974
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APPLICATION NUMBER: 60/056,893
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APPLICATION NUMBER: 60/056,662
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APPLICATION NUMBER: 60/056,880
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APPLICATION NUMBER: 60/056,637
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EARLIER PELLING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,894
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/057,669
FILING DATE: 1997-09-05
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APPLICATION UNDBER: 60/056,664
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,876
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APPLICATION NUMBER: 60/056,875
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APPLICATION NUMBER: 60/056,862
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/048,964
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APPLICATION NUMBER: 60/057,650
FILING DATE: 1997-09-05
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APPLICATION NUMBER: 60/043,670
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APPLICATION NUMBER: 60/056,909
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APPLICATION NUMBER: 60/056,887
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APPLICATION NUMBER: 60/056,881
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APPLICATION NUMBER: 60/047,593
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FILING DATE: 1997-08-22
APPLICATION WUMBER: 60/056,911
ELING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,636
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APPLICATION NUMBER: 60/056,874
FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,845
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APPLICATION NUMBER: 60/056,892
FILING DATE: 1997-08-22
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,590
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APPLICATION NUMBER: 60/047,594
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APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments TITLE OF INVENTION: Learment of infection FILE REFERENCE: 9710-003-99
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 111
LENGTH: 940
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TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
CURRENT PELLIGE DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
                                                                                                                                                                                                                                                                                                                          6; Mismatches
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EARLIER PILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
EARLIER APPLICATION NUMBER: 60/048,880
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EARLIER FILING DATE: 1997-06-06
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Pred. No.
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,876
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APPLICATION NUMBER: 60/048,895
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APPLICATION WUNBER: 60/048,884
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,894
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILLING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILLING DATE: 1997-10-02
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Patent No. 6525174
GENERAL INFORMATION:
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Best Local Similarity 40.7%;
Matches 11; Conservative
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Best Local Similarity
Matches 12; Conserv
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US-09-198-452A-111
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GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZOO7P1
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CURRENT PELLING DATE: 1998-12-04

CURRENT FILING DATE: 1998-12-04

EARLIER APPLICATION NUMBER: UT/US98/11422

EARLIER APPLICATION NUMBER: 60/048,885

EARLIER FILING DATE: 1997-06-06

EARLIER FILING DATE: 1997-06-06
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BARLIER FILING DATE: 1997-06-06
BEARLIER FILING DATE: 1997-06-06
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BEARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER APPLICATION NUMBER: 60/048,915
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BEARLIER FILING DATE: 1997-06-06
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BEARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
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R APPLICATION NUMBER: 60/048,971
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,964
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,882
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APPLICATION NUMBER: 60/048,899
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,893
FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,895
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APPLICATION NUMBER: 60/048,884
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,894
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Patent No. 6525174
                                    7 VRWAFESLQVPQNRPERWASH 27
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BARLIER FILING DATE: 1997-06-06

BARLIER APPLICATION NUMBER: 60/048,971

EARLIER FILING DATE: 1997-06-06

BARLIER APPLICATION NUMBER: 60/048,964

BARLIER APPLICATION NUMBER: 60/048,989

EARLIER APPLICATION NUMBER: 60/048,899

EARLIER APPLICATION NUMBER: 60/048,899

EARLIER APPLICATION NUMBER: 60/048,993

EARLIER FILING DATE: 1997-06-06

EARLIER PILING DATE: 1997-06-06

EARLIER PLING DATE: 1997-06-06

EARLIER PILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,991

EARLIER FILING DATE: 1997-06-06

EARLIER PILING DATE: 1997-06-06

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EARLIER APPLICATION NUMBER: 60/048,991

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EARLIER PILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER PILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER PILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
SAGURWARE: PALENT NOWER: 60/094,657
SOFTWARE: PALENT NEW DATE: 1998-07-16
SQTWARE: PALENT NEW DATE: 1998-07-16
SQTWARE: PALENT NEW DATE: 1998-07-16
SQTWARE: PALENT NEW DATE: 1998-07-16
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EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-205-258-646
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Length 654; Indels

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Query Match
25.3%; Score 48.5; DB 3;
Best Local Similarity 25.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 12; Mismatches 9;
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          NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REPERENCE/DOCKET NUMBER: 2307K-0624000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEPHONE: 415-326-2402
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
LENGTH: 654 amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 SYRYKLINWAYQQ----VQQNKEDAWIEHDVWR 31
                                                                                                                                                                                                                                                                                                                                                                                                  ; IOCATION: 1..654
; OTHER INFORMATION: /note= "consensus"
US-08-560-005-10
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Job time: 21.9535 secs
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Region
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LOCATION: (105)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: SITE
LOCATION: (115)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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APPLICANT: Pot, David A.
APPLICANT: Williams, Lewis T.
APPLICANT: Williams, Lewis T.
APPLICANT: Majerus, Philip W.
TITLE OF INVENTION: No. 6001354el Grb2 Associating Protein and Nucleic TITLE OF INVENTION: Acids Encoding Therefor NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS: 20
ADDRESSEE: Townsend and Townsend and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,005
                        BARLIER APPLICATION NUMBER: 60/048,897
BARLIER FILING DATE: 1997-06-06
BARLIER FILING DATE: 1997-06-06
BARLIER PLING DATE: 1997-07-12-18
BARLIER PLING DATE: 1997-07-15
BARLIER PLING DATE: 1998-07-15
BARLIER PLING DATE: 1998-07-30
          APPLICATION NUMBER: 60/048,883
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US-08-560-005-10
Sequence 10, Application US/08560005
Partent No. 6001354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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STATE: California
COUNTRY: USA
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LENGTH: 120
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July 12, 2004, 13:51:07 ; Search time 74.7209 Seconds
(without alignments)
128.567 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1 RRSYRYKLINWAYQQVQQNKEDAWIEHDVWRMEI 34
                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                1586107 seqs, 282547505 residues
                                                                                                                                                                                  US-10-010-667A-2_COPY_185_218
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Maximum Match 100%
Listing first 45 summaries
                                                                          - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		σ.	_	Aab75315 Human sec	₩.	6 STEAE	'n	σ.			Abu98389 Novel hum	4	Novel	Abu98387 Novel hum	Abu98393 Novel hum	Novel		Novel		Novel	Novel]	Novel]	Novel]	Novel	Abu98399 Novel hum	Abu98398 Novel hum
SUMMARIES	ID		AAY58199	AAE02787	AAB75315	AAB75314	ABU98426	ABU98425	ABU98429	ABU98428	ABU98395	ABU98389	ABU98424	ABU98392	ABU98387	ABU98393	ABU98390	ABU98391	ABU98384	ABU98431	ABU98396	ABU98397	ABU98394	ABU98388	ABU98386	ABU98399	ABU98398
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Abu60886 Human G p	Human	Abu98432 STEAP-1 v	Abu98427 STEAP-1 v	Abu98385 Novel hum		Aam01282 P789P ami		Aam78845 Human pro		Abb95387 Human P78		Abu98383 Novel hum		Abu98430 STEAP-1 v	Abr54499 Prostate	Abu63313 Human six	Adb75573 Prostate	Adb14329 Human pro	Aae02780 Human six
ABU60886	ABU60887	ABU98432	ABU98427	ABU98385	AAY58194	AAM01282	AAU69927	AAM78845	ABU71818	ABB95387	ABG61813	ABU98383	ABU98414	ABU98430	ABR54499	ABU63313	ADB75573	ADB14329	AAE02780
9	9	9	9	9	n	4	4	4	4	2	2	9	9	9	9	7	_	7	4
267	267	282	282	282	339	339	339	339	339	339	339	339	339	339	339	339	339	339	375
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
192	192	192	192	192	192	192	192	192	192	192	192	192	192	192	192	192	192	192	192
26	27	28	56	30	31	32	33	34	35	36	37	38	36	40	41	4.2	4 6	44	45

ALIGNMENTS

RESULT 1 AAY58199

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Serpentine transmembrane antigen of the prostate; STRAP-1; prostate; transmembrane domain; type IIIa membrane protein; expression; cancer; prostate cancer; bladder cancer; colon cancer; parcreatic cancer; ovarian cancer; tumour antigen; immunisation; immune response; cellular; humoral; anticancer vaccine; antibody; detection; diagnosis; prognosis; monitoring; susceptibility; therapeutic inhibitor; drug targetting;
                                                                Human STRAP-1 peptide, corresponding to STRAP-1 extracellular region 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel proteins useful as diagnostic markers and therapeutic targets, particularly for prostatic cancer.
                                                                                                                                                                                                                                                                                                                                                                                                              DC;
                                                                                                                                                                                                                                                                                                                                                                                                              Saffran
                                                                                                                                                                                                                                                                                                                                                                                                               Raitano AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 22; 83pp; English.
 AA.
                                                                                                                                                                                                                                                                                                                                                                                                               Leong K,
AAY58199 standard; peptide; 34
                                                                                                                                                                                                                                                                       99WO-US012157.
                                                                                                                                                                                                                                                                                           98US-0087520P.
98US-0091183P.
                                              (first entry)
                                                                                                                                                                                                                                                                                                                             (UROG-) UROGENESYS INC.
(AFAR/) AFAR D E.
(HUBE/) HUBERT R S.
                                                                                                                                                                                                                                                                                                                                         AFAR D E.
HUBERT R S.
LEONG K.
RAITANO A B.
SAFFRAN D C.
                                                                                                                                                                                                                                                                                                                                                                                                                Hubert RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-072832/06.
                                                                                                                                                                 recombinant protein.
                                                                                                                                                                                       Synthetic.
Homo sapiens.
                                                                                                                                                                                                                                                                     01-JUN-1999;
                                                                                                                                                                                                                         WO9962941-A2
                                                                                                                                                                                                                                                                                            01-JUN-1998;
30-JUN-1998;
                                             14-MAR-2000
                                                                                                                                                                                                                                               09-DEC-1999,
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                        AAY58199;
                                                                                                                                                                                                                                                                                                                                                                             (RAIT/)
(SAFF/)
                                                                                                                                                                                                                                                                                                                                                                   (LEON/)
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6 6 6 7

Sequences AAYS8198-Y58200 represent synthetic peptides that correspond the extracellular regions of STRAP-1 (serpentine transmembrane antigen

WPI; 2001-367804/38.

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the professe, AAYSB194. These peptiates were used to raise monocional anti-STRAP-1 antibodies, STRAP-1 is the prototype member of the STRAP-1 curtural conservation, but which show no significant structural extructural conservation, but which show no significant structural conservation, but which show no significant structural chromosome 7p22. STRAP-1 is thought to be a type IIIa membrane protein chromosome 7p22. STRAP-1 is a 339 amino acid protein characterised by six transmembrane domains and intracellular N- and C-termini, suggesting that it folds in a "serpentine" manner into three extracellular and two intracellular and throughout all stages of protein characterised by six and/or protein is also overexpressed in certain other cancers, including chief in a leader, color, pancreatic and ovarian cancer. The function of the STRAP protein is not known. They may be ion channels (from the presence of six transmembrane domains, a feature which is shared by certain ion channels) or gap-junction proteins (from immunohistochemical staining). STRAP-1 and syptems in munical staining). STRAP-1 and syptems in munical staining or cell-surface thus used to identify specific-binding protein induces cell-surface thusour antigenes. Immunication with a STRAP-1 and munical staining of cancers (or susceptibility to cancer), as therapeutic modulations or to target therapeutic agents to their site of action. STRAP concined acids may be used for recombinant protein production, as calls for screening inhibitions of STRAP expression since high levels of STRAP proteins are exposed on the cell surface, they are easily targetted by systemically administered agents they are easily targetted by systemically administered agents transpected to them should have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, cytostatic, antiproliferative, vaccine; gene therapy; six transmembrane epithelial antigen of the prostate-1, STEAP-1; chromosome 7p22.3; cancer; prostate; colon; bladder; pancreatic; ovarian; lung; extracellular loop; serpentine transmembrane antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Extracellular loop #2 of human STEAP-1, suitable for cloning into pFc.
  prostate, AAY58194). These peptides were used to raise monoclonal
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Jakobovits A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 34 AA;
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The present invention relates to human six transmembrane epithelial antigen of the prostate (STEAP) protein. STEAP is a member of cell surface serpeitine transmembrane antigens. STEAP gene is used in gene therapy. Inhibiting the development or progression of a cancer (eg. prostate, color, bladder, lung, ovarian and pancreatic) expressing STEAP or inhibiting growth or killing cells expressing STEAP in a patient. Treating a vaccine composition to the patient. Treating a patient with a cancer that expresses STEAP, or inhibiting growth or killing cells expressing STEAP, comprises administering to the patient of killing cells expressing STEAP, comprises administering to the patient accordence ancoding single chain monoclonal antibody that comprises the variable domains of the heavy and light chains of the monoclonal antibody that chains of the monoclonal antibody coding sequence to the cancer cells and the encoded single chain monoclonal antibody is expressed the cancer cells and intracellularly. The present sequence is extracellular loop of STEAP-1 surfable for cloning into PFC, which is used in the invention. STEAP-1 cere antipolar page of the chomosome 7P22.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                        New STEAP (six transmembrane epithelial antigen of the prostate)
proteins, expressed in human cancers, useful for detecting and treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiproliferative, cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective; antibacterial; virucide, fungicide; opthalmalogical; vulnerary; autoimmune disease; hyperproliferative disorder; cardiovascular disorder; cerebrovascular disorder; cerebrovascular disorder; ocerbrovascular disorder; ocerbrovascular disorder; chemotaxis; food additive; nervous system disorder; ocular disorder; chemotaxis; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; immunosuppressive; antiarthritic; antirheumatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted protein sequence encoded by gene 20 SEQ ID NO:134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 192; DB 4;
Pred. No. 3.8e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RRSYRYKLLNWAYQOVQONKEDAWIEHDVWRMEI 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RRSYRYKLINWAYQQVQQNKEDAWIEHDVWRMEI 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                   Example 19; Page 102; 187pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Komatsoulis GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB75315 standard; protein; 129 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2000; 2000WO-US015135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC. (ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0138632P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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Best Local Similarity 100.
Matches 34, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-071257/08.
N-PSDB; AAF63808.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200077021-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JUN-1999;
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This invention relates to polynuclectide sequences AAF63836
which encode human secreted proteins AAB75260 - AAB75287. Included in the
invention are protein sequences AAB75288 - AAB75341 which are fragments
of the secreted proteins and amino acid sequences with which these
cf fragments share homology. Examples of the activities of the proteins and
polynuclectides and the activities of their agonists and antagonists
include, immunosuppressive; autianthritic; antirheumatic;
antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
condropic; neuroprotective; antibacterial; virucide; fungicide;
copthalmalogical; and vulnerary activity. The protein and polynucleotide
sequences, their agonists and antagonists may be useful for treating,
coptasms of the breast or liver, cardiovascular disorders e.g.
chisases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.
chisases of the breast or liver, cardiovascular disorders e.g. cardiac
arrest, cerebrovascular disorders e.g. cardiac
cartest, cerebrovascular disorders e.g. cerebral ischaemaia, anglogenesis,
cartest, cerebroides can also be used to aid wound healing and epithelial
colliproprides can also be used to aid wound healing and epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiproliferative, cytostatic, cardiant, vasotropic, cerebroprotective, neuroprotective, antibacterial; virucide, fungicide, opthalmalogical, vulnerary; autoimmune disease, hyperproliferative disorder; cardiovascular disorder, cerebrovascular disorder, infection, nervous system disorder; ocular disorder; chemotaxis; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell proliferation, to prevent skin aging due to sumburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. Included in the invention are oligonucleotides AAPF63780 - AAPF63788 and peptide AABP5239 which are used in the identification and characterisation of the DNA and protein sequences of
           Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene 20 human secreted protein homologous amino acid sequence #133.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; immunosuppressive; antiarthritic; antirheumatic; nootropic;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 192; DB 4; 100.0%; Pred. No. 1.8e-18; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 RRSYRYKLLINWAYQQVQQNKEDAWIEHDVWRMEI 93
                                                                                                    Disclosure; Page 53-54; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB75314 standard; protein; 129 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    secreted protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 129 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200077021-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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This invention relates to polynucleotide sequences AAF63789 - AAF63836
which encode human secreted proteins AAB75260 - AAB75287. Included in the
invention are protein sequences AAB75289 - AAB75341 which are fragments
of the secreted proteins and amino acid sequences with which these
cf fragments share homology. Examples of the activities of the proteins and
polynucleotides and the activities of their agonists and antagonists
cf fragment since include, immunosuppressive; antiarthritic; antirheumatic;
antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
cnotropic; neuroprotective; antiarthritic; antirheumatic;
antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
coptialmalogical; and vulnerary activity. The protein and polynucleotide
coptialmalogical; and vulnerary activity. The protein and polynucleotide
csquences, their agonists and antagonists may be useful for treating,
preventing and diagnosing diseases and disorders such as autoimmune
cc sequences, themedotid arthritis, hyperproliferative disorders e.g.
creplasms of the breast or liver, cardiovascular disorders e.g.
creplasms of the breast or liver, cardiovascular disorders e.g.
creplasms of the breast or liver, cardiovascular disorders e.g.
creplasms of the breast or liver, cardiovascular disorders e.g.
creplasms of the breast or liver, cardiovascular disorders e.g.
creprotein, viruses and fungi and ocular disorders e.g. corneal infection.
Cc arrest, creprorection, to prevent skin aging due to sumburn, to maintain
cc cell proliferation, for prevent skin aging due to sumburn, to maintain
cc calls be used as a food additive or preservative to innocrase or decrease
cc storage capabilities. Included in the invention are oligomucleotides
cc therefore the and characterisation of the DNA and protein sequences of
the billication and characterisation of the DNA and protein sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STEAP-1; six transmembrane epithelial antigen of the prostate; cancer; cancer vaccine; delineation; cytogenetic abnormality; cytostatic;
                                                                                                                                                Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 100.0%; Score 192; DB 4; Length 129; Local Similarity 100.0%; Pred. No. 1.8e-18; nes 34; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RRSYRYKLINWAYQQVQQNKEDAWIEHDVWRMEI
                                                                                                                                                                                                                                              Disclosure; Page 53-54; 530pp; English.
                                                               Komatsoulis GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABU98426 standard; protein; 254 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-SEP-2002; 2002WO-US028371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STEAP-1 variant 8P1D4 v.2 #2.
(HUMA-) HUMAN GENOME SCI INC.
(ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                 Ruben SM,
                                                                                                           WPI; 2001-071257/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 129 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003022995-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU98426;
                                                                   Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
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Gaps

01-JUN-2000; 2000WO-US015135.

21-DEC-2000

99US-0138632P.

11-JUN-11999;

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The invention describes a composition comprising a substance that modulates the status of a protein (I) of 340 or 283 amino acids, or of any of the 15 sequences of 259 amino acids, given in the specification, or a molecule that is modulated by the protein, where the status of the polynucleotides and methods are useful for treating and detecting cancer. The STEAR-1-related proteins are useful for generating cancer vaccines. The polynucleotides are useful for delineating value are useful for penerating cancer vaccines. Precision, cytogenetic abnormalities in the chromosomal region that encodes STEAR-1 that may contribute to the malignant phenotype. This is the amino acid sequence of a variant of human six transmembrane epithelial antigen of the prostate or STEAR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STEAP-1; six transmembrane epithelial antigen of the prostate; cancer; cancer vaccine; delineation; cytogenetic abnormality; cytostatic;
                                                                                                                                 New composition comprising a substance that modulates the status of STEAP-1-related protein, useful for treating and detecting cancer.
                                                                            Challita-Eid PM, Jakobovits A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jakobovits A;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 192; DB 6; 100.0%; Pred. No. 3.8e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RRSYRYKLINWAYQQVQQNKEDAWIEHDVWRMEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                           Example 53; Page 169-170; 248pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABU98425 standard; protein; 254 AA.
                                                                          Ge W, Raitano AB,
06-SEP-2001; 2001US-0317840P.
05-APR-2002; 2002US-0370387P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STEAP-1 variant 8P1D4 v.1 #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-SEP-2001; 2001US-0317840P. 05-APR-2002; 2002US-0370387P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-JUL-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34; Conservative
                                             (AGEN-) AGENSYS INC.
                                                                                                     WPI; 2003-313240/30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AGEN-) AGENSYS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 254 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003022995-A2.
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                                                                         Faris M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU98425;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Faris M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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New composition comprising a substance that modulates the status of STEAP-1-related protein, useful for treating and detecting cancer.

Example 53; Page 169-170; 248pp; English.

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Gaps

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Indels

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The invention describes a composition comprising a substance that modulates the status of a protein (1) of 340 or 283 amino acids, or of any of the 15 sequences of 259 amino acids, given in the specification, or a molecule that is modulated by the protein, where the status of the cell that expresses the protein is modulated. The compositions, proteins, polynucleotides and methods are useful for treating and detecting cancer. The polynucleotides are useful for generating cancer vaccines. The polynucleotides are useful as tools for delineating, with greater precision, cytogenetic abnormalities in the chromosomal region that encodes STRAP-1 that may contribute to the malignant phenotype. This is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention describes a composition comprising a substance that modulates the status of a protein (1) of 340 or 283 amino acids, or of any of the 15 sequences of 259 amino acids, given in the specification, or a molecule that is modulated by the protein, where the status of the polymucleorides and methods are useful for treating and detecting cancer. The polymucleorides and methods are useful for generating cancer vaccines. The polymucleotides are useful as tools for delineating, with greater precision, cytogenetic abnormalities in the chromosomal region that encodes STEAP-1 that may contribute to the malignant phenotype. This is the amino acid sequence of a variant of human six transmembrane epithelial antigen of the prostate or STEAP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STEAP-1; six transmembrane epithelial antigen of the prostate; cancer; cancer vaccine; delineation; cytogenetic abnormality; cytostatic;
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New composition comprising a substance that modulates the status of STEAP-1-related protein, useful for treating and detecting cancer.
                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                           Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jakobovits A;
                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                   ch 100.0%; Score 192; DB 6; Similarity 100.0%; Pred. No. 3.8e-18; 34; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                   185 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Challita-Eid PM,
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                                                                                                                                                                                                                            epithelial antigen of the prostate or STEAP-1
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2002US-0370387P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-313240/30.
                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                 Sequence 254 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-SEP-2001;
05-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JUL-2003
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ABU98429
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GENERAL INFORMATION:

APPLICANT: LINE OR INVENTION: NUCELEC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT PAPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-0
PRIOR FILING DATE: 1997-10-14
RICR APPLICATION NUMBER: US 60/065,779
PRIOR FILING DATE: 1997-10-14
RICR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
SEQ ID NO 5.278
LENGTH: 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: No. 6605280ick, Daniela
APPLICANT: Diazello, Charles
APPLICANT: Experation, Menachem
APPLICANT: Expiratello, Charles
TITLE OF INVENTION: Use
FILE REFERENCE: 20993-001
FILE REFERENCE: 20993-001
CURRENT PAPLICATION NUMBER: US/09/485,632B
FRIOR APPLICATION NUMBER: 1198/00379
FRIOR APPLICATION NUMBER: 1298-08-13
FRIOR FILING DATE: 1998-07-12
FRIOR FILING DATE: 1998-07-22
FRIOR PAPLICATION NUMBER: 122134
FRIOR FILING DATE: 1997-11-06
FRIOR FILING DATE: 1997-11-06
FRIOR FILING DATE: 1997-11-06
FRIOR FILING DATE: 1997-11-06
FRIOR FILING DATE: 1997-09-29
FRIOR FILING DATE: 1997-09-29
FRIOR FILING DATE: 1997-08-27
FRIOR FILING DATE: 1997-08-27
FRIOR PRILING DATE: 1997-08-27
FRIOR FILING DATE: 1997-08-27
FRIOR PRILING DATE: 1997-08-27
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                                                                                                                                                                                                Score 43; DB 4; Length 278;
Pred. No. 17;
                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5278, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-485-632B-6; Sequence 6, Application US/09485632B; Patent No. 6605280
                                                                           LENGTH: 278
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                        50.0%;
  1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |:||| | :||:||
234 KVKPRNN-KEDNYL 246
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Best Local Similarity 64.3.
Lag 9; Conservative
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Best Local Similarity 53.8<sup>†</sup>
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                               2 KMKPRRNLEEDDY 14
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PRIOR FILLING DATE: 19
NUMBER OF SEQ ID NOS:
SEQ ID NO 11367
                                                                                                                                                          US-09-489-039A-11367
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US-09-134-001C-5278
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Patent No. 6610836
GENERAL INFORMATION
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
OF INVENTION:
FILE OF INVENTION:
FILE REPRENCE:
2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE:
2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
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JEQUENCE 6624, Application US/09134000C

Sequence 6624, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn DOUCETE-Stamm et al

APPLICANTO: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: PATENTIN VETSION 3.1
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                        APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Oatrer, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Walg, Aijun
APPLICANT: Hepler, William
ITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: UNAGNOSIS OP PROSTATE CANCER
FILE REFERENCE: 210121.427C21
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FastSRQ for Windows Version 3.0
IENGTH: 339
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100.0%; Pred. No. 1.5e-06;
tive 0; Mismatches 0; Indels
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Best Local Similarity 61.5%; Pred. No. 4;
Matches 8; Conservative 3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 WKMKPRRNLEEDDYL 28
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125 IKPKRYLEEGDYI 137
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        Retter, Marc W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens US-09-685-166A-879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
''hee 15, Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-489-039A-11367
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LENGTH: 216
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Sequence 879, App
Sequence 6624, Ap
Sequence 11367, A
Sequence 527, Ap
Sequence 6, Appli
Sequence 54, Appli
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5168, Ap
4, Appli
2, Appli
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Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 6, Appli
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Sequence 6422, Ap
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                                                                                                                         July 12, 2004, 14:04:08; Search time 9.24419 Seconds (without alignments) 83.770 Million cell updates/sec
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(cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

(cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

(cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-685-166A-879

US-09-685-166A-879

US-09-489-039A-11367

US-09-134-001C-5278

US-09-485-632B-6

US-09-247-373B-54

US-09-252-991A-3134

US-09-51379-4

US-09-51379-4

US-09-51379-4

US-09-51379-4

US-09-104-276-5168

US-09-134-000C-4765

US-09-134-000C-4765

US-09-134-000C-4765

US-09-134-000C-4765

US-09-107-532A-6422

US-09-651-99A-7

US-09-651-976-523

US-08-61-376-5

US-08-489-7461

US-09-489-7461

US-09-489-7461

US-09-489-7461

US-09-489-039A-13425

US-08-338-125-4

US-08-338-126-4
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                                                                                                                                                                                                                                                                                                                                                                       389414 seqs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
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                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Sequence 879, Application US/09685166A
PARTEN NO. 6630305
GENERAL INFORMATION:
APPLICANT: XU, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Gary R.

1 WKMKPRRNLEEDDYL 15

14 WKMKPRRNLEEDDYL

US-09-685-166A-879

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                                    49, Appl
49, Appl
24, Appl
13, Appl
2, Appl
2, Appl
82, Appl
82, Appl
6, Appl
4, Appl
4, Appl
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6, Appl
6, Appl
6, Appl
6, Appl
7, Appl
6, Appl
6, Appl
7, Appl
7, Appl
8, Appl
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Sequence 13, A
Sequence 2, Ap
Sequence 2, Ap
Sequence 82, A
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                                 Sequence 49,
Sequence 49,
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Sequence 2, Application US/09323873A

Sequence 2, Application US/09323873A

Sequence 3. Applicant

APPLICANT: Daniel E. Afar

APPLICANT: Rene S. Hubert

APPLICANT: Rahan Leong

APPLICANT: Arbur B. Raitano

APPLICANT: Steve Chappell Mitchell

TITLE OF INVENTION: NOVEL SERFENTINE TRANSMEMBRANE ANTIGENS

ITLE OF INVENTION: EXPENSESED IN HUMAN CANCERS AND USES THEREOF

FILE REPERENCE: 129.16USU2

CURRENT APPLICATION NUMBER: US/09/323,873A

CURRENT APPLICATION NUMBER: 60/087,520

PRIOR APPLICATION NUMBER: 60/087,520

PRIOR PLING DATE: 1998-06-01

PRIOR PLING DATE: 1998-06-30

PRIOR PLING DATE: 1998-06-30

PRIOR PLING DATE: 1998-06-30
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Sequence
Sequence
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US-08-834-108-6
US-09-446-301A-49
US-08-484-105-24
US-08-484-106-24
US-08-76-317-13
US-09-314-645-2
US-09-243-560B-2
US-09-344-645-2
US-09-536-784-82
US-09-536-784-82
US-09-536-784-82
US-09-536-784-82
US-09-402-929-6
US-09-402-929-6
US-09-439-313-537
US-08-834-108-4
US-08-439-313-537
US-09-688-166A-537
US-09-688-166A-537
US-09-688-166A-537
US-09-688-166A-537
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 339
  464
522
522
572
577
605
711
711
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Best Local Similarity 100.
Matches 15, Conservative
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US-09-323-873A-2
                                                                               US-09-323-873A-2
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Mon Jul 12 15:36:42 2004

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Search completed: July 12, 2004, 14:27:48 Job time : 26.5116 secs

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HAFILCANT: Walanabe, Yoshiniro
HAPPLICANT: Deng, Ta
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REPERENCE: 210121.42728
CURRENT APPLICATION NUMBER: US/10/144,678A
CURRENT FILING DATE: 2002-08-12
MUMBER OF SEQ ID NOS: 1033
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 879
LENGTH: 339
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APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C29
CURRENT APPLICATION NUMBER: US/10/294,025
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 1038
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 879
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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Houghton, Raymond L.
Vinals y de Bassols, Carlota
Foy, Teresa M.
Watanabe, Yoshihiro
Deng, Ta
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                                                       Experience of the state of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Skeiky, Yasir A. W. Hepler, William T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 WKMKPRRNLEEDDYL 15
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Best Local Similarity 100.0
These 15; Conservative
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Best Local Similarity 100.0
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang, Aijun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens US-10-144-678A-879
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US-10-294-025-879
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US-10-294-025-879
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APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gannavarapu, Manjula
APPLICANT: Garbaccheva, Bella
APPLICANT: Garbaccheva, Bella
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Monsey, Angela M.
APPLICANT: Monsey, Angela M.
APPLICANT: Monsey, Angela M.
APPLICANT: Monsey, Novel Genes, Compositions, Kits, AND
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHADS FOR IDENTIFICATION, ASSESSMENT, PREVENTION OF THE REPERENCE: MILOGOP-25
TITLE OF INVENTION: WINDER: 60/307,982
CURRENT APPLICATION NUMBER: 60/314,356
PRIOR FILING DATE: 2001-09-22
PRIOR PELICATION NUMBER: 60/314,746
PRIOR FILING DATE: 2001-109-22
PRIOR PELICATION NUMBER: 60/314,746
PRIOR FILING DATE: 2001-10-12
PRIOR PILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-10-12
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PRIOR PILING DATE: 2001-10-12
PRIOR PILING DATE: 2001-12-12
PRIOR PILING DATE: 2001-10-12
PRIOR PILING DATE: 2001-10-12
PRIOR PILING DATE: 2001-10-12
PRIOR PILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/342,158
PRIOR PILING DATE: 2001-10-12
PRIOR PILING DATE: 2001-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
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US-10-144-678A-879
; Sequence 879, Application US/10144678A
; Publication No. US20030157089A1
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Publication No. US20030108963A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Endege, Wilson O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 WKMKPRRNLEEDDYL 15
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                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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Matches 15; Conserv
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US-10-205-823-397
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Sequence 2, Application US/10010667A
; Sequence 2, Application US/20030055217A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Daniel
; APPLICANT: Hubert, Rene S.
; APPLICANT: Heong, Kahan
; APPLICANT: Saffran, Douglas C.
; APPLICANT: Mitchell, Steve Chappell
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THERBOF
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THERBOF
; FILE REPERENCE: 511582001601
; CURRENT FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/087,520
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                                                                                          100.0%; Score 86; DB 13; Length 339; 100.0%; Pred. No. 2e-05; Live 0; Mismatches 0; Indels
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Best Local Similarity 100.0
Matches 15; Conservative
                                                                                                              Best Local Similarity 100.
Matches 15; Conservative
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; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-896-879
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US-10-010-667A-2
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                                                                                                  Query Match
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                            US-10-408-009-6

; Sequence 2, Application US/10408009
; Publication No. US20040072196A1
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Arthur B. Raitano
; APPLICANT: Arthur B. Raitano
; APPLICANT: Stephen C. Mitchell
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; TITLE OF INVENTION: WOVEL S. US/10/408, 009
; CURRENT APPLICATION NUMBER: US/10/408, 009
; CURRENT FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/455, 486
; PRIOR APPLICATION NUMBER: 09/323, 873
; NUMBER OF SEQ ID NOS: 36
; SOFFWARE: RastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LEMATH: 339
; TUNDE: DEPT
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APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 879, Application US/10012896; Publication No. US20020183251A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C. APPLICANT: Mitcham, Jennifer L. APPLICANT: Harlocker, Susan L. APPLICANT: Jiang, Yuqiu APPLICANT: Kalos, Michael D. APPLICANT: Retter, Marc W. APPLICANT: Stolk, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang, Aijun
Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
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Vedvick, Thomas S.
Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 210121.427C27
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Matches 15; Conserv
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US-10-012-896-879
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                          US-10-408-009-2
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APPLICANT:
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APPLICANT:
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SEQ ID NO 13
LENGTH: 339
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APPLICANT: Forger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FRSESO for Windows Version 3.0
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                                                                                                               100.0%; Score 86; DB 9; Length 339; 100.0%; Pred. No. 2e-05; ive 0; Mismatches 0; Indels
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                                 ) NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020187472A1 g6572948
US-09-802-520-11
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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                                                                                                                                                                                                                                                                                                                           ; Sequence 879, Application US/09895793; Publication No. US20020192763A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Giang, Yuqiu
APPLICANT: Kales, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
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Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
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Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
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ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-09-895-793-879
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Matches 15; Conserva
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Sequence 13, Application US/10205267

Sequence 13, Application US/10205267

Sequence 13, Application US/10205267

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Spancake, Kimberly M.
APPLICANT: Spancake, Kimberly M.
APPLICANT: Ison, Craig H.
ITILE OF INVENTION: TRANSMEMBRANE PROTEIN DIFFERENTIALLY EXPRESSED IN PROSTATE AND ITILE OF INVENTION: TUMORS
FILE REFERENCE: PV-0008 CIP
CURRENT APPLICATION NUMBER: US/10/205,267

CURRENT APPLICATION NUMBER: US/10/205,267

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PERL PROGram
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APPLICANT: Forger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 879
LENGTH: 339
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DATABASE ACCESSION NUMBER: Genbank ID No: g6572948

US-10-205-267-13
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McNail, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
Foy, Teresa
                                                                                                                                                                    Wang, Aijun
Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
                                                                               Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Jiang, Yuqiu
Kalos, Michael D.
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                                     Retter, Marc W.
Stolk, John A.
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Best Local Similarity 100.0
Matches 15, Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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US-09-895-814-879
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Gaps

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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hepler, William
APPLICANT: Hebler, William
APPLICANT: Houghton, Barricia D.
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSRQ for Windows Version 3.0
SEQ ID NO 879
LENGHH: 339
TYPE: PRT
ORGANISM: Homo sapiens
US-09-780-669-879
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; Sequence 879, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION UNUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 879
; LENGTH: 3339
; TYPE: PRT
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Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels
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Sequence 11, Application US/09802520
Publication No. US20020187472A1
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Taris, Marx,
APPLICANT: Ison, Craig H.
TITLE OF INVENTION: STEAP-RELATED PROTEIN
FILE REFERENCE: PC-0037 US
CURRENT APPLICATION OF THE CO-0037 US
UNMBER OF SEQ ID NOS: 11
SOUTHWARE: PERL PROGRAM
SEQ ID NO 11
LENTH: 339
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US-09-822-827-879
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Matches 15; Conserv
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US-09-822-827-879
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APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.427C23

CURRENT APPLICATION NUMBER: US/09/759,143

CURRENT FILING DATE: 2001-01-12

NUMBER OF SEQ ID NOS: 934
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100.0%; Pred. No. 2e-05;
tive 0; Mismatches 0; Indels
             ch 100.0%; Score 86; DB 14; Length 15; L Similarity 100.0%; Pred. No. 1e-06; 15; Conservative 0; Mismatches 0; Indels
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Patent No. US20020051977A1
GENERAL INFORMATION:
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
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Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
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Wang, Aijun
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Matches 15; Conserv
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US-09-780-669-879
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US-09-759-143-879
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16: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                           US-10-010-667A-2_COPY_14_28
86
1 WEXEPRILEEDDYL 15
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES)-165	-759-	-780-	-822-	-802-	895-	895-	-205	-408	-013	-011	-010	1 6	202-6	-144	US-10-294-025-879
SU	ID	US-10-165-044-22	JS-09-759-143-879	US-09-780-669-879	JS-09-822-827-879	-60-S	US-09-895-793-879	US-09-895-814-879	US-10-205-267-13	US-10-408-009-2	118-10-012-896-879	US-10-011-095-2	118-10-010-6678-2		US-10-202-823-33/	US-10-144-678A-879	US-1(
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Semience 37, Appl	714	Segmence 1347. An	7277			Sequence 130585.		Sequence 60. Appl	Sequence 128802.	Sequence 165124.	Sequence 13, Appl	Sequence 204350,	Sequence 17721. A	Segmence 32, Appl	Sequence 76. Appl	Sequence 2. Appli	Sequence 63876. A	Sequence 67, Appl	Segmence 43994. A	Sequence 259292.	43788	203.	203	203	203	203	203	203	Sequence 203, App
US-10-239-607-37	us-	us-	US-	US-		US-	US-10-424-599-2	US-10	US-10-437-963-128802					US-09-801-574-32	US-09-801-574-76	US-10-132-861-2	US-10-425-114-63876	US-10-158-034-67	US-10-425-114-43994	US-10-424-599-259292	\simeq	US-10-671-403-203	US-10-671-419-203	US-10-670-844-203	-10	-10-673-098-	-10-672-638-	-10-	US-10-670-817-203
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100.0	100.0	100.0	100.0	100.0	53.5	52.3	51.2	51.2	50.0	50.0	50.0	48.8	48.8	48.8	48.8	48.8	48.8	48.3	48.3	48.3	48.3	47.7	47.7	47.7	47.7	47.7	47.7	47.7	47.7
96	98	98	98	98		45		44	43	43	43	42	42		42	42	42	41.5	41.5	41.5	41.5	41	41	41	41	41	41	41	41
16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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RESULT 1

US-10-165-044-22

Sequence 22, Application US/10165044

Publication No. US20030149531A1

GENERAL INFORMATION:

APPLICANT: Rene S. Hubert

APPLICANT: Rene S. Hubert

APPLICANT: Apalas Saffran

APPLICANT: Dauglas Saffran

APPLICANT: Dauglas Saffran

APPLICANT: Apalaboruts

TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF

FILE REFERENCE: 51158-20016, 02

CURRENT APPLICATION NUMBER: US 60/091,183

PRIOR FILING DATE: 1998-06-01

PRIOR FILING DATE: 1998-06-01

PRIOR FILING DATE: 1999-06-01

PRIOR APPLICATION NUMBER: US 09/455,486

PRIOR FILING DATE: 1999-06-01

PRIOR APPLICATION NUMBER: US 09/455,486

PRIOR FILING DATE: 1999-06-01

PRIOR FILING DATE: 1999-06-01

PRIOR PRILING DATE: 1990-06-01

PRIOR PRINCE PRINCE
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GenCore version 5.1.6
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- protein search, using sw model OM protein

July 12, 2004, 14:01:53 ; Search time 7.5 Seconds (without alignments) 192.383 Million cell updates/sec Run on:

US-10-010-667A-2_COPY_14_28 86

1 WKMKPRRNLEEDDYL 15 score: Seguence: Perfect

283366 segs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SUPERSTANCE	Description		ribonuclease III	RNase D, processes	RNase D, processes		cal p		hage	hypothetical	hypothetical	dihydrolipoam					ABC-type tran			hypothetical p	transcription				retinoic	xCRABP - Afri	hypothetical	hypothetical		
a o o		T50202	NRECD	A99943	E85791	T02539	T15371	T39150	AH1754	T49020	D96692	D36718	T49021	JC4836	AC2594	D97376	875010	C84550	G75287	T21493	T46637	F71258	876909	EDBEGA	B31872	151265	T49337	T23899	T00943	
	DB	5	Н	7	N	~	~	0	7	7	7	N	7	7	7	7	~	~	N	0	~	7	N	Н	7	7	7	~	7	
	Length	237	375	375	375	532	312	539	124	384	416	442	451	847	1832	1858	260	271	403	580	1187	639	658	1415	36	138	361	430	474	
	% Query Match	52.9		52.3	52.3	51.2	50.0	50.0	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	47.7	47.7	47.7	47.7	47.7	47.1	47.1	47.1	46.5			46.5	46.5	
	core	45.5		45	45	44	43	43	42	42	42	42	42	42	42	42	41	41	41	41	41	40.5	40.5	40.5	40	40	40	40	40	
	Result No.	1	N	m	4	Ŋ	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	

		hypothetical prote	hypothetical prote	probable Ogr famil	probable activator	isocitrate dehydro	pyruvate dehydroge	protein T2E6.2 [im	hypothetical prote	transcription regu	hypothetical prote	probable calmodul1	poly (beta-D-mannur	۲	dve protein - irui
F69361	H83322	T01167	T18955	H90665	C85516	C64499	E83981	B96519	G89841	B69764	T23035	B84568	JC5870	A97104	T00117
н	7	7	7	~	7	7	7	7	~	7	7	~	7	7	7
549	884	961	1268	90	90	371	426	426	449	479	512	652	713	916	1019
46.5	46.5	46.5	46.5	45.3	45.3	45.3	45.3	45.3	45.3	45.3	45.3	45.3	45.3	45.3	45.3
40	40	40	40	39	39	39	39	39	39	39	39	39	39	39	39
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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conserved hypothetical protein SPAC25B8.15c [imported] - fission yeast (Schizosaccharomy, conserved hypothetical protein SPAC25B8.15c [imported] - fission yeast (Schizosaccharomy, C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
C;Accession: TSO202
A;Reference number: 225045
A;Accession: TSO202
A;Accession: TSO202
A;Accession: TSO202
A;Accession: TSO202
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A;Accession: SPACSSSO TSO203
A;Accession: SPACSSSO TSO303
A;Accession: SPACSSSO TSO303
A;Accession: SPACSSSO TSO303
A;Accession: SPACSSSO TSO303325; PIDN:CAB61781.1; GSPDB:GN00066; SPDB:SPAC25B8.15c
A;Experimental source: strain 972h(-); cosmid c25B8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Genetics:
A;Gene: SPDB:SPAC25B8.15c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 1
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52.9%;

Gaps 1; 2; Length 237; Indels 3, Score 45.5; DB Pred. No. 4.3; Mismatches Conservative Query Match Best Local Similarity Matches 10; Conserva

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Tibounclease III (EC 3.1.26.3) rnd - Escherichia coli (strain K-12)
N.Alternate names: ribonuclease D
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 30-Unu-1991 #sequence revision 30-Jun-1991 #text_change 01-Mar-2002
C;Date: 30-Unu-1991 #sequence revision 30-Jun-1991 #text_change 01-Mar-2002
C;Accession: S01223; A30431; S41590; D64941; S42849; D21915
R;Zhang, J.; Deutscher, M.P.
Nucleic Acids Res. 16, 6265-6278, 1988
A;Title: Escherichia coli RNase D: sequencing of the rnd structural gene and purification A;Reference number: S01223; MUID:88289400; PMID:3041371

A;Molecule type: DNA A;Residues: 1-375 <ZHA> A;Cross-references: EMBL:X07055; NID:g42770; PIDN:CAA30098.1; PID:g581215 A;Accession: A30431

A,Molecule type: protein
A,Residues: 1-6 <ZH2.
B,Fulda, M.; Heinz, E.; Wolter, F.P.
Mol. Gen. Genet. 242, 241-249, 1994
A;Fulda, M.; Heinz, E.; Wolter, F.P.
A;Fulda, M.; Heinz, E.; Wolter, F.P.
A;Fule: The fadd gene of Escherichia coli K12 is located close to rnd at 39.6 min of t.
A;Reference number: 841588; MUID:94150456; PMID:8107670
A;Molecule type: DNA

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C,Accession: E85791
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayh iller, Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, B.; Potamousis, K.; Apodac, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                            A;Accession: E85791
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-375 < STO>
A;Cross-references: GB:AE005174; NID:g12515844; PIDN:AAG56793.1; GSPDB:GN00145; UMGP:Z
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein At2g37730 [imported] - Arabidopsis thaliana

NyAlternate names: hypothetical protein F13M22.23

Cybecass Arabidopsis thaliana (mouse-ear cress)

Cybecassion: T02539; #sequence_revision 05-Mar-1999 #text_change 16-Feb-2001

CyAccession: T02539; D84796

RyRounaley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, Submitted to the EMBL Data Library, June 1998

A;Reference number: Z14677

A;Reference mumber: Z14677

A;Reference mumber: Z14677

A;Residues: 1-532 <ROLS

A;Re
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
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A,Introns: 165/2; 295/3; 478/3
C,Superfamily: Arabidopsis hypothetical protein F13M22.23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein COIF1.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
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Pred. No. 8.5;
2; Mismatches
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ilarity 63.6%;
Conservative
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A,Gene: rnd
C,Superfamily: ribonuclease D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                342 WKLKPQNNLPE 352
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tes 7; Conserv
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Best Local Similarity
Matches 10; Conserv
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   Across-references: GB:X70994; NID:g433478; PIDN:CAA50322.1; PID:g581071
A; Experimental source: strain K12
R; Blattner, R.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc. A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-375 <BLAT>
A;Cross-references: GB:AE000274; GB:U00096; NID:G1788089; PIDN:AAC74874.1; PID:G1788105;
A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Riffayashi, T.: Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res: B, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gence A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E85791
RNase D, processes tRNA precursor [imported] - Escherichia coli (strain O157:H7, substra
C;Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNase D, processes tRNA precursor [imported] - Escherichia coli (strain 0157.H7, substra
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A,Molecule type: DNA
A,Eesidues: 1-375 <HAY>
A,Cross-references: GB:BA000007, PIDN:BAB35936.1; PID:g13361980; GSPDB:GN00154
A,Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                            A; Accession: D64941 A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Species: Bscherichia coli
C.Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C.Accession: A99943
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Pred. No. 8.5;
2; Mismatches 2; Indels
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C;Superfamily: ribonuclease D
C;Keywords: exonuclease; hydrolase
F;1-375/Product: ribonuclease D #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted to the EMBL Data Library, February 1993
A;Reference number: 842848
A;Accession: 842849
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 'L',2.38 <FUZ>
A;Cross-references: EMBL:X70994
C;GeneLios:
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Pred. No. 8.5;
2; Mismatches
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C;Superfamily: ribonuclease D
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Matches 7; Conservative
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hypothetical protein F3C22.70 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: T49920
R;Purnelle, B.; Masuy, D.; Goffeau, A.; Boutry, M.; Mewes, H.W.; Rudd, S.; Lemcke, K.; hsubmitted to the Protein Sequence Database, April 2000
A;Reference number: Z25013
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C;Species Arabidopsis thaliana (mouse-ear cress)
C;Decies Arabidopsis thaliana (mouse-ear cress)
C;Decies Arabidopsis thaliana (mouse-ear cress)
C;Decies G. Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: D96692
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Coway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hulzar, L.
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziall, Rizzo, M.; Rooney, T.; Sowhartz, J.R.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, A;Reference and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MulD:21016719; PMID:11130712
A;Accession: D96692
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A;Cross-references: GB:AL592022; PIDN:CAC97808.1; PID:g16415103; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin2581
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A;Cross-references: EMBL;AL353912; GSPDB:GN00061; ATSP:F3C22.70
A;Experimental source: cultivar Columbia; BAC clone F3C22
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                                                                                                                                                                                        Length 124;
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Pred. No. 31;
3; Mismatches
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8.6;
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                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                Score 42;
Pred. No.
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                                                                                                                                                                                                Query Match
Best Local Similarity 46.7%;
Matches 7; Conservative
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15 WKRKRKKILRRDEYL 29
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Best Local Similarity 50.0
Matches 7; Conservative
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A, Introns: 61/1; 252/3; 281/3
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Best Local Similarity
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A, Status: preliminary
A, Molecule type: DNA
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A;Gene: T1217.9
A;Map position: 1
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C;Species: Listeria innocus
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
B; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mayauthors: Kreft, J.; Simose, N.; Tererez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Reference number: AB1077; MuID:21537279; PMID:11679669
A;Accession: AH1754
A;Accession: AH1754
A;Accession: L24 <GLA>
       C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999 C;Accession: T15371
R;Johnson, D.
R;Johnson, D.
R;Johnson, D.
R;Johnson, D.
R;Johnson, D.
R;Johnson, D.
R;Reference number: Z1833
R;Accession: T15371
A;Reference number: Z1833
A;Accession: T15371
A;Reference number: Z1833
A;Accession: T15371
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-312 < JOHN.
A;Residues: 1-312 < JOHN.
A;Residues: 1-312 < JOHN.
A;Residues: T1-312 < JOHN.
A;R
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bacteriophage protein homolog lin2581 [imported] - Listeria innocua (strain Clip11262)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable heat shock transcription factor - fission yeast (Schizosaccharomyces pombe)
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A;Molecule type: DNA
A;Residues: 1-539 <OLI>
A;Cross-references: EMBL:Z99168; PIDN:CAB16301.1; GSPDB:GN00066; SPDB:SPACBC9.14
A;Experimental source: strain 972h-; cosmid c8C9
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C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
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A;Reference number: Z21748
A;Accession: T39150
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Pred. No. 27;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.0%; Score 43; DB 2; Length 312; 63.6%; Pred. No. 15; 2; Indels :ive 2; Mismatches 2; Indels
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A;Map position: 1
A;Introns: 10/3; 40/3; 67/2; 86/3
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Best Local Similarity 60.0%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     || | :||||:
PRTNKQEDDYI 260
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Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Introns: 36/2; 271/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: CESP: C01F1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: T39150
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alpha-glucuronidase (EC 3.2.1.-) precursor - fungus (Trichoderma reesel)
NiAleznate names: GLRI
C;Specias: Trichodeama reesel
C;Date: 15-Aug-1996 #sequence_revision 15-Oct-1996 #text_change 03-Nov-2003
C;Accession: U74836
R;Margolles-Clark, B.; Saloheimo, M.; Siika-aho, M.; Penttilae, M.
Gene 172, 171-172, 1996
A;Title: The alpha-glucuronidase-encoding gene of Trichoderma reesei.
A;Reference number: JC4836; MUID:96257277; PMID:8654984
A;Reference number: JC4836; MUID:96257277; PMID:8654984
A;Recession: U46836
A;Molecule type: mRNA
A;Residues: 1-847 < MAR>
A;Residues: 1-847 < MAR>
A;Residues: 1-847 < MAR>
A;Gene: glrl
C;Genetics:
C;Genetics: G;Genetics: G;Genetics: G;Reywords: glrcuronidase
C;Genetics: G;Reywords: glrcuronidase
C;Genetics: G;Reywords: glrcuronidase
C;Reywords: glrl
C;Superfamily: alpha-glucuronidase
C;Reywords: glrcuronidase
C;Reywords: glrcuronidase
C;Reywords: glrcuronidase
F;20-847/Product: alpha-glucuronidase #status predicted <NAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-1832 <KUR>
A; Cross-references: GB: AE008688; PIDN: AAL41169.1; PID: g17738468; GSPDB: GN00186
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A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens
A,Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48.8%; Score 42; DB 2; Length 847; 53.8%; Pred. No. 65;
                  A; Experimental source: cultivar Columbia; BAC clone F3C22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42; DB 2; 1
Pred. No. 1.4e+02;
                                                                                                                                                                                                          DB
33;
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                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                          Score 42;
Pred. No.
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                                                                                                                                                                                                       48.8%;
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108 KLSPKINLKEDGY 120
                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 KMKPRRNLEEDDY 14
                                                                                                        A;Map position: 3
A;Introns: 4/2; 294/3; 339/3
                                                                                                                                                                                                                                                                                                                                                                                    52 WKLVPNLEFDSDDY
                                                                                                                                                                    Ouery Match
Best Local Similarity
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                                                  C;Genetics:
A;Gene: ATSP:F3C22.80
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A, Status: preliminary
A, Molecule type: DNA
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                                                                                                                                                                                                                   Altyworkouploamande S. Dacetyltransterase (EC 2.3.1.12) precursor - Bacillus subtilis of Species: Bacillus subtilis dehydrogenase complex, E2 component C. Species: Bacillus subtilis dehydrogenase complex, E2 component C. Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 20-Jun-2000 C. Accession: D36718; B66674

N. Bacteriol. 172, 5052-5063; 1990

A; Title: Secretory S. Complex of Bacillus subtilis: sequence analysis and identity to pyr A; Accession: D36718; MUD:9036658; PMID:1697575

A; Residues: preliminary

A; Molecule type: DNA

A; Residues: Date: Miller, S.; Bruschi, C. V.; Caldwell, B.; Capuano, V.; Carter, N.M.; ChA

A; Escience: Bron, S.; Bruschi, C. V.; Caldwell, B.; Capuano, V.; Carter, N.M.; ChC, S.; Entrich, S. D.; Emmerson, P. T.; Entian, K. D.; Errington, V.; Fabret, C.; Ferrari, B.; Entrich, S. D.; Emmerson, P. T.; Entian, K. D.; Errington, V.; Puna, S.; Galler, N.; Entrich, S. D.; Emmerson, P. T.; Hibert, H.; Holsappel, S.; Hosono, S.; Hullo, M. F. A; Entrich, S. D.; Emmerson, P. T.; Hibert, H.; Holsappel, S.; Hosono, S.; Hullo, M. F. A; Entrich, S. D.; Emmerson, P. T.; Minner, S.; M.; Parro, V.; Pohl, T. M.; Pottetelle A; M.; Valodes, M.; Kurine, A.; Liu, H.; Masuda, S.; Mauthors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sezonion, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sezonion, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Pasper, M.; Tamake, H.; Parro, V.; Puna, K.; Yosanion, A; Attheres, P.; Wippt, A.; Yamanok, M.; Willers, P.; Wippt, A.; Yamanok, M.; Willers, P.; Wippt, A.; Yamanok, M.; Willers, P.; Wippt, A.; Yamanok, M.; Pamakeshi, A.; Tamaka, H.; Panchin, A.; Tosato, V.; Vochiyama, A; A; Reference number: A65580; MUD:98044033; PMID:938437;
A; Accession: B65674
A; Residues: T. A; Residues of the Gram-pomponion tot shown
A; Residues: T. A
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A; Residues: 1.142 < KUN>
A; Cross-references: GB:299111; GB:AL009126; NID:g2633699; PIDN:CAB1333.1; PID:g2633831
A; Experimental source: strain 168
A; Ganetics: C; Superfamily: dihydrolipoamide acetyltransferase; lipoyl/biotin-binding homology C; Keywords: acyltransferase; coenzyme A; oxidoreductase
C; Keywords: acyltransferase; coenzyme A; oxidoreductase
E; 4-77/Domain: lipoyl/biotin-binding homology < LPB>
F; 4-77/Domain: lipoyl/biotin-binding homology < LPB>
F; 4-77/Domain: lipoyl/biotin-binding homology < LPB>
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Clate: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
Clatesolon: T49021
Riburnelle, B.; Masuy, D.; Goffeau, A.; Boutry, M.; Mewes, H.W.; Rudd, S.; I submitted to the Protein Sequence Database, April 2000
A;Reference number: Z25013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-451 < PUR>
A; Cross-references: EMBL: AL353912; GSPDB:GN00061; ATSP:F3C22.80
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                                                                                                                                                                                                       dihydrolipoamide S-acetyltransferase (EC 2.3.1.12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48 84; Scor.
46.78; Pred. No. 33,
... 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 WFVKPNDEVDEDDVL 36
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   WKMKPRRNLEEDDY 14
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                                  40 WKYVPRLDLDEADF
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Best Local Similarity
Matches 7; Conservat
                                                                                                                                                 RESULT 11
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Length 1832;

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GENERAL INFORMATION:
APPLICANT: ADAMS, Mark
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, THEREOF
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
FILE REPERENCE: CL001381
CURRENT PILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SOFTWARE: PATES
TYPE: PRT
TYPE: PRT
TYPE: PRT
TYPE: PRT
CORGANISM: Homo sapiens
US-10-170-205E-14765
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48.8%; Score 42; DB 6; Length 996;
Best Local Similarity 53.8%; Pred. No. 96;
Matches 7; Conservative 2; Mismatches 4; Indels
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APPLICANT: ADAMS, Mark
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
FILE REPERBING: CLOOD 381
CURRENT APPLICATION NUMBER: US/10/170, 205E
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: Patentin version 3.2
SEQ ID NO 14827
                                                                                                                                                                                                                                                                                             GENURAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Calo, Yihua
APPLICANT: Calo, Yougwei
APPLICANT: Calo, Yougwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT APPLICATION NUMBER: US/20/4-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 44432
LENGTH: 817
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Pred. No. 78;
1; Mismatches 3; Indels
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Score 42; DB 6; Length 331;
Pred. No. 30;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C45757_1.pep
US-10-767-701-44432
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Pred. No. 86;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/FEX: unsure
NAME/FEX: unsure
OTHER INFORMATION: unsure at all Xaa locations
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; Sequence 14765, Application US/10170205E
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US-10-170-205E-14827
Sequence 14827, Application US/10170205E
GENERAL INFORMATION:
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         48.8%;
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                                                                                                                                                                                        233 WEMAKRSNLSEDE 245
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Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                1 WKWKPRRNLEEDD 13
               Query Match
Best Local Similarity 53.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Sorghum bicolor
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, ORGANISM: Homo sapiens
US-10-170-205E-14827
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Best Local Similarity
...c 7; Conserva
                                                                                                                                                                                                                                                                                RESULT 13
US-10-767-701-44432
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TITLE OF INVENTION: MEGALIN-BASED DELIVERY OF THERAPEUTIC COMPOUNDS TO THE BRAIN AND TITLE OF INVENTION: OTHER TISSUES
TITLE OF INVENTION: OTHER TISSUES
TITLE OF INVENTION: OTHER TISSUES
CURRENT APPLICATION NUMBER: US/10/812,849
CURRENT APPLICATION NUMBER: US/10/812,849
PRIOR PLING DATE: 2004-03-30
PRIOR PLING DATE: 2003-06-20
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTION NUMBER: 203-06-20
LUMBER OF SEQ ID NOS: 29
SOFTWARE: Atentin version 3.2
LENGTH: 331
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TITLE OF INVENTION: DELIVERY OF THERAPEUTIC COMPOUNDS TO THE BRAIN AND OTHER TISSUES

FILE REPERENCE: 30610/39383 PCT/US04/19153

CURRENT APPLICATION NUMBER: PCT/US04/19153

CURRENT FILING DATE: 2004-06-23

PRIOR APPLICATION WIMBER: US 10/600,862

PRIOR FILING DATE: 2003-06-20

NUMBER OF SEQ ID NOS: 29

SOFTWARE: Patentin version 3.2
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Pred. No. 19;
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Pred. No. 30;
2; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                     CURRENT FILING DATE: 2003-12-01
PRIOR APPLICATION NUMBER: 09/450,969
PRIOR PILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: 09/134,001
PRIOR PILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: 60/064,964
PRIOR PILING DATE: 1997-11-08
PRIOR PILING DATE: 1997-10-08
PRIOR PILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 7544
SEQ ID NO 5260
LENGTH: 256
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234 KVKPRNN-KEDNYL 246
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Best Local Similarity 53...
7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 64.3
Matches 9; Conservative
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US-10-724-972A-5260
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ORGANISM: Zebrafish
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ORGANISM: Zebrafish
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US-10-812-849-25
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LENGTH: 331
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US-10-724-972A-5260
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US-10-752-421-35
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APPLICANT: Rene S. Hubert

APPLICANT: Arthur B. Raitano

APPLICANT: Stephen C. Mitchell

ITILE OF INVENTION: NOVEL SERENTINE TRANSMEMBRANE ANTIGENS

TITLE OF INVENTION: NOVEL SERENTINE TRANSMEMBRANE ANTIGENS

TITLE OF INVENTION: NOVEL SERENTINE TRANSMEMBRANE ANTIGENS

TITLE REFERENCE: 51158/2001607

CURRENT APPLICATION NUMBER: US/10/857,785

CURRENT FILING DATE: 1999-105-20

PRIOR PRILICATION NUMBER: US 09/455,486

PRIOR PRILICATION NUMBER: US 09/323,873

PRIOR PILING DATE: 1999-06-01

PRIOR FILING DATE: 1998-06-01

PRIOR FILING DATE: 1998-06-01

PRIOR FILING DATE: 1998-06-01

NUMBER OF SEQ ID NOS: 47

SOFTWARE: FESTSEQ for Windows Version 4.0
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APPLICANT: Rene S. Hubert
APPLICANT: Parlur B. Raiteno
APPLICANT: Arthur B. Raiteno
APPLICANT: Arthur B. Raiteno
APPLICANT: Oudglas C. Saffran
APPLICANT: Stephen C. Mitchell
APPLICANT: Stephen C. Mitchell
APPLICANT: Stephen C. Mitchell
APPLICANT: Stephen C. Mitchell
APPLICANT: STEPHENCE: STEPHENCE: STEPHENCE
TITLE OF INVENTION: NOVEL SERVENCED IN HUMAN CANCERS AND USES THEREOF
CURRENT APPLICATION NUMBER: US, 10,965,109
CURRENT FILING DATE: 2004-05-28
PRIOR APPLICATION NUMBER: US 09/455,486
                                                                                                                                                                                                                               100.0%; Score 86; DB 6; Length 349; 100.0%; Pred. No. 1.1e-06; Live 0; Mismatches 0; Indels
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CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SEQ ID NO 18326
LENGTH: 349
                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-857-785-35; Sequence 35, Application US/10857785; CENERAL INFORMATION; APPLICANT: Daniel E. Afar; APPLICANT: Rene S. Hubert
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US-10-856-109-35
; Sequence 35, Application US/10856109
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                 15; Conservative
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US-10-170-205E-18326
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 15; Conserv
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LENGTH: 16
                                                                                                                                       TYPE: PRT
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Best Local
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Sequence 5260, Application US/10724972A

GENERAL INFORMATION:

APPLICANT: DOUGCTG-Stamm, Lynn

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: PATHO3-16

CURRENT APPLICATION NUMBER: US/10/724,972A
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APPLICANT: Bene S. Hubert
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Stephen C. Mitchell
TITLE OF INVENTION: NOVEL SERENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
TITLE REPERENCE: 511582001612
CURRENT APPLICATION NUMBER: US/10/752,421
CURRENT FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: US 09/455,486
PRIOR APPLICATION NUMBER: US 09/323,873
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: US 60/091,183
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93.8%; Pred. No. 2.5e-06;
live 0; Mismatches 0;
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93.8%; Pred. No. 2.5e-06;
live 0; Mismatches 0;
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: US 09/323,873
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: US 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 35
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Best Local Similarity 93.83
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-10-856-109-35
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ORGANISM: Homo sapiens
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CURRENT FILING DATE: 2004-05-28
PRIOR APPLICATION NUMBER: US 09/455,486
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: US 09/323,873
PRIOR FILING DATE: 1999-06-01
PRIOR PELING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
SOFTWARE: FASTERQ FOR WINDOWS VERSION 4.0
SOFTWARE: FASTERQ FOR WINDOWS VERSION 4.0
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Best Local Similarity 100.0
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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CORGANISM: Homo sapiens
US-10-856-109-2
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US-10-170-205E-18326
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APPLICANT: Rene S. Hubert
APPLICANT: Arthur B. Raitert
APPLICANT: Arthur B. Raitert
APPLICANT: Arthur B. Raitert
APPLICANT: Stephen C. Mitchell
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 511582001606
CURRENT APPLICATION NUMBER: US/10/856,109
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                                                                                                                                                                                                               100.0%; Score 86; DB 6; Length 339; 100.0%; Pred. No. 1e-06; 1. Indels 1. Indels
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                ; PRIOR APPLICATION NUMBER: PCT/USO1/09410
; PRIOR FILING DATE: 2001-03-23
; PRIOR FILING DATE: 2000-03-24
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 339
; TYPE: PRT
; CREANISM: Homo sapiens
US-10-239-607A-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/10856109 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                      1 WKMKPRRNLEEDDYL 15
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Best Local Similarity 100.
Matches 15; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-10-856-109-2
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GENERAL INFORMATION:
APPLICANT: ADAMS, MARK
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
FILE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
FILE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
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APPLICANT: Arbura B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Douglas C. Mitchel
APPLICANT: Stephen C. Mitchel
TITLE OF INVENTION: BERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REPRENCE: 511582001612
CURRENT APPLICATION NUMBER: US/10/752,421
CURRENT FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: US 60/6401.05
PRIOR APPLICATION NUMBER: US 60/097,520
PRIOR APPLICATION NUMBER: US 60/097,520
PRIOR APPLICATION NUMBER: US 60/097,520
PRIOR PRILING DATE: 1998-06-01
PRIOR PRILING DATE: 1998-06-01
PRIOR PRILING DATE: 1998-06-01
PRIOR PRILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-01
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100.0%; Score 86; DB 6; Length 339; 100.0%; Pred. No. 1e-06;
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118.046 Million cell updates/sec
                                                                                                                                      July 12, 2004, 14:08:08; Search time 9.4186 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                     OM protein - protein search, using sw model
                                                                                                                                      Run on:
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US-10-010-667A-2_COPY_14_28 86 Perfect score: Title:

1 WKMKPRRNLEEDDYL 15 Seguence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

393080 seqs, 74121830 residues Searched:

393080 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pending Patents AA New:*

1: /cgn2 6/ptcdata/2/paa/JPCT NEW COMB.pep:*

2: /cgn2 6/ptcdata/2/paa/JBC6 NEW COMB.pep:*

3: /cgn2 6/ptcdata/2/paa/JBC0 NEW COMB.pep:*

4: /cgn2 6/ptcdata/2/paa/JBC0 NEW COMB.pep:*

5: /cgn2 6/ptcdata/2/paa/JBC0 NEW COMB.pep:*

6: /cgn2 6/ptcdata/2/paa/JBC0 NEW COMB.pep:*

7: /cgn2 6/ptcdata/2/paa/JBC0 NEW COMB.pep:*

7: /cgn2 6/ptcdata/2/paa/JBC0 NEW COMB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	į	ednence	Sequence 37, Appl	2.	equence 2.	ì	emience 183	, L) (equence 35	100		equence 25,	444	14007	17051	E 2 2 2 7	Semience 5641 Ap	2037,	, ,	Segmence 23732	27475	10/113	16541	747	1011	
SUMMARIES	ID		-T0-071-80T-/	-10-239-607A-3	-10-857-	-826-	US-10-752-421-2	US-10-170-205E-18326		-109 - 3	0-752-421-3	-724-972A-	JS04-19153-25	2-849-25	. 4	10-170-205E-1	- 1	-60-581-351-563	51-564	-964B-2	06-203	170-205E-2	-248-796A-214	790-338B-6	US-10-170-205E-16541	-767-471-744	7-471-74	-170-205
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APPLICANT: Saatcioglu, Fahri TITLE OF INVENTION: Novel Prostate-Specific or TITLE OF INVENTION: Testis-Specific Nucleic Acid Molecules, Polypeptides, and TITLE OF INVENTION: Diagnostic and Therapeutic Methods TITLE REPREBENCE: 50218(003002 CURRENT APPLICATION UNMER: US/10/239,607A

; Sequence 37, Application US/10239607A; GENERAL INFORMATION:

RESULT 2 US-10-239-607A-37

14 WKWKPRRNLEEDDYL 28

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Section 100 appears			Semience 3/22, Ap		Semience 848 App		Semience 27413 A	105		200		Somioned 11000, A	440	Sequence 23, Appl	sednence 37, Appl	Seguence 32. Appl	Seminary 100		12/00	Sequence 357, App
US-10-767-471-747	US-10-170-205E-27412	US-60-556-841-5722	US-10-767-471-745	US-10-767-471-750	US-10-821-801-848	US-10-767-471-749	US-10-170-205E-27413	PCT-US03-24982A-125	US-60-551-161-260	US-60-565-632-11886	US-60-579-062-11886	TIS-10-170-205E-24904	US-60-546-745-03	DCT-TTG04-1900A-30	7C-476CT-4050-173	US-10-873-467-32	US-60-551-121-100	US-60-581-13766	DD 77 H D 100 C C C C C L L L L L L L L L L L L L L	FCI-0202-22838A-35/
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27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	,	7.	43	44	4.5)

ALIGNMENTS

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Gaps
                                                                                                                                                                                         APPLICANT: SOURCY, LARGEAN
APPLICANT: RODGE, Stefan
APPLICANT: Mennerich, Detlev
APPLICANT: Kinneman, Henrik
APPLICANT: Li, Xinzhong
TITLE OF INVENTION: Human nucleic acid sequences from lung tumours
FILE REFERENCE: 00154/00201
CURRENT APPLICATION NUMBER: US/10/821,801
PRIOR APPLICATION NUMBER: DE 103 16 701.3
PRIOR APPLICATION NUMBER: DE 103 16 701.3
NUMBER OF SEQ ID NOS: 900
SOFTHARE: Patentin version 3.2
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                  Sequence 741, Application US/10821801 GENERAL INFORMATION:
                                                                                                                                    Pilarsky, Christian
Brummendorf, Thomas
                                                                           Rosenthal, Andre
Hermann, Klaus
Heiden, Esmeralda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 WKMKPRRNLEEDDYL 15
                                                       APPLICANT: Hinzmann, Bernd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                           Staub, Eike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo Sapiens
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Best Local Similarity
Matches 15; Conserv;
US-10-821-801-741
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APPLICANT:
APPLICANT:
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LENGTH: 339
                                                                           APPLICANT:
APPLICANT:
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APPLICANT:
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Dysylothetical protein AGR_C_235 [imported] - Agrobacterium tumefaciens (strain C58, Cered C5pecies: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: D97376
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, Science 294, 2323-2328, 2001
A;Iilu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume; A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1658 cKUR>
A;Crossreferences: GB:AE007869; PIDN:AAK85965.1; PID:g15155024; GSPDB:GN00169
C;Genetics:
A;Gene: AGR_C_235
A;Map position: circular chromosome
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      3; Indels
      3; Mismatches
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356 LRPLRTVETDDYL 368
7; Conservative
Matches
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Search completed: July 12, 2004, 14:11:17 Job time : 8.5 secs

3 MKPRRNLEEDDYL 15 ::| |:| ||| 382 LRPLRTVETDDYL 394

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                                      46.5%; Score 40; DB 1; Length 549;
46.2%; Pred. No. 46;
Live 4; Mismatches 3; Indels
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Pred. No. 46;
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         123 "HIGH" REGION.
62861 MW; 39DF41CC0B9AD210 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00324; aa permeases; I. PROSITE; PS00218; AMINO_ACID_PERWEASE_1; FALSE_NEG.
                                                                                                                                                                     15-UUL-1999 (Rel. 38, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Putative polyamine transporter.
                                                                                                                                                   553 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
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60633 MW;
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                            Ouery Match
Best Local Similarity 46.27
Best Local Similarity 6.27
                                                                             1 WKMKPRRNLEEDD 13
                                                                                                                                                                                                             GPT1.
Candida albicans (Yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 WKMKPRRNLEEDD 13
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TRANSMEM 43 63
                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
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549 AA;
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Best Local Similarity
Matches 6; Conserv
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                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NGTLSLSCVÄCSRFPNFSILYMLGNGSFIEHLPGRLW --> SWAEGNLAPHPRSPALQPQQSTAAGLRLSTGPAAAQP (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VRSPRRGLOEGEELCFHMWGGKGGLCOSSL -> AGLRATL
PPTQEALPSSHSSPQQQG (in isoform A).
 "Interleukin-18 binding protein: a novel modulator of the Th1 cytokine
                                                                                                                                                                                                                                                   Xiang Y., Moss B.;
"Identification of human and mouse homologs of the MC51L-53L-54L
family of secreted glycoproteins encoded by the Molluscum contagiosum
                                                                                                                                                                                                                                                                                                                    Vivology 257:297-302(1999).
-!- FUNCTION: Binds to IL-18 and inhibits its activity. Functions as an inhibitor of the early TH1 cytokine response.
-!- SUBCELLUAR LOCATION: Secreted (Potential).
-!- ALTERNATIVE PRODUCTS:
                                                     [2]
SEQUENCE FROM N.A. (ISOFORM A), SEQUENCE OF 29-33; 37-43; 46-52;
55-58; 61-72; 89-93; 105-142 AND 149-167, AND TISSUE SPECIFICITY.
MEDINE-99192308; PubMed-10094485;
Alzawa Y., Akita K., Taniai M., Torigoe K., Mori T., Nishida Y.,
Ushio S., Nukada Y., Tanimoto T., Ikegami H., Ikeda M., Kurimoto M.;
"Cloning and expression of interleukin-18 binding protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=B; Synonyms=IL-18BPB;
IsoId=095998-3; Sequence=VSP 002515, VSP 002516;
TISSUE SPECIFICITY: Strongly expressed in heart, lung, placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunogiobulin domain; Giycoprotein; Signal, Alternative splicing.

SICNAL

28
GIYCOPROTEIN; SIGNAL

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10-FIRE CZ-TYPE.

DOWALN

63
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SYSIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and spleen.
-!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60; G0:0005625; C:soluble fraction; TAS.
60; G0:0042007; F:interleukin-IB binding; IDA.
60; G0:0004811; F:signal transducer activity; TAS.
60; G0:0006955; P:immune response; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                         Name=C: Synonyme=IL-18BPC;
Isode=O95998-1; Sequence=Displayed;
Name=A; Synonyme=IL-18BPC;
Name=A; Synonyme=IL-18BPA;
Name=A; Synonyme=IL-18BPA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AP110798; AAD17187.1; ...
EMBL; AF110798; AAD17188.1; ...
EMBL; AF110799; AAD17189.1; ...
EMBL; AF110799; AAD17189.1; ...
EMBL; AF110801; AAD17191.1; ...
EMBL; AP110801; AAD17192.1; ...
EMBL; AR10801; AAD7374.1; ...
EMBL; AF122966; AAD41051.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         isoform B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTIG=VSP
                                                                                                                                                                                                                                 MEDLINE=99263157; PubMed=10329540;
                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR007110; Ig-like.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                 FEBS Lett. 445:338-342(1999).
                        response.";
Immunity 10:127-136(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HGNC:5987; IL18BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77
92
101
145
197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM; 604113;
                                                                                                                                                                                                                                                                                                       poxvirus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genew;
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Pfam; PF03485; N-Arg; 1.
Pfam; PF035746; LRNA-synt_1d; 1.
PRINTS; PR01038; TRNA-SYNTHARG.
TIGRAPMs; TIGR00456; args; 1.
PROSITE; PS00178; AA_TRNA_LIGASE I; FALSE NEG.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Kel. 41, Last annotation update)
Arginyl-TRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS)
ARGS OR AF0894.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 390:364-370(1997).

-!- CATALYTIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP + diphosphate + L-arginyl-tRNA(Arg).

-!- SUBGELLULAR LOCATION: Cytoplasmic.

-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=VC-16 / DSM 4304 / ATCC 49558;
MBDLINE=98049343; PubMed=9894975;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.B., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loffus B.,
Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L
Overbeek R., Gocapha D., Weidman J.F., McDonald L., Utterback T.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
                                                                                                                                                                                                                        .;
0
                                                                                                                                                 46.5%; Score 40; DB 1; Length 197; 46.7%; Pred. No. 16;
                                                                                                                                                                                                                        Indels
Missing (in isoform B).
Frid=VSP 002516.
FIDE626AB2B285E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea; Buryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAMAÞ; MF 00123; -; 1.
InterPro; IPR001278; Arg_tRNA-synt_lc.
InterPro; IPR005148; N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR008909; tRNA-synt_ld_C.
InterPro; IPR001412; tRNA-synt_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE001042; AAB90346.1; -. PIR; F69361; F69361.
                                                                                        21698 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Created)
                                                                                                                                                                                                                                                                                                                               1 WKMKPRRNLEEDDYL 15
                                                                                                                                                                                 Best Local Similarity 46.7
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaeoglobus fulgidus.
                     197
                                                                                     197 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIGR; AF0894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYR_ARCFU 029368;
                 VARSPLIC
                                                                                        SEQUENCE
                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
SYR_ARCFU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WARRAND DRAWN DRAW
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RET3 XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                I18B HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INIT MET
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                            P50568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IL18BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     I18B HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
                           Q
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0
                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                     ogatus garias (circus).
Bukaryota, Metazoa, Chodata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kitamoto T., Momoi T., Momoi M.;

Biochem. Biophys. Res. Commun. 159:371-371(1989).

-I- FUNCTION: CYTOSOLIC CRABBS MAY REGULARE THE ACCESS OF RETINOIC ACID TO THE NUCLEAR RETINOIC ACID RECEPTORS.

-I- FUNCTION: CRABP-II MAY PARTICIPATE IN A REGULATORY FEEDBACK MECHANISM TO CONTROL THE ACTION OF RETINOIC ACID ON CELL
                                                                                                                                                                                                                                                                                                                                                                                                                   protein in
                                                                                                                                                                                                                                                      01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Retinoic acid-binding protein II, cellular (CRABP-II) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- TISSUE SPECIFICITY: Embryo.
-!- SIMILARITY: Belongs to the fatty-acid binding protein (FABP)
                                                                                                                                       i,
EMBL, M75729; AAA46111.1; -.
InterPro; IRR005205; Herpes ICP4 C.
InterPro; IRR005205; Herpes ICP4 N.
Pfam; PF03585; Herpes ICP4 C; 1.
Pfam; PF03584; Herpes ICP4 N; 1.
Barly protein; Transcription regulation; Trans-acting factor; Activator; DNA-binding; Phosphorylation; Nuclear protein.
DOMAIN 155 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                 DB 1; Length 1415;
                                                                                                                                                                                                                                                                                                                                                                                                   Kitamoto T., Momoi T., Momoi M.;
"The presence of a novel cellular retinoic acid-binding prochick embryos: purification and partial characterization.";
                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40; DB 1; Length 36; Pred. No. 2.5;
                                                                                          C0846F7BEF4D1126 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2BC1C154B2FD9904 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.
                                                                                                               47.1%; Score 40.5; DB 1
60.0%; Pred. No. 1e+02;
iive 2; Mismatches
                                                                                                                                                                                                                                     36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR, B31872, B31872.
HSSP, P29373; 1CBS.
InterPro; IRR00463; Fatty acid BP.
InterPro; IRR00566; Lipocln_cyfFABP.
Pfam; PF00061; lipocalin; 1.
PROSITE; PS0214; FABP; 1.
                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=89087453; PubMed=2849937;
                                                                             155 200 SER
                                                                                                                                                                      46.5%;
                                                                                                                                                         2 KMKPR-RNLEEDDYL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 AA; 3997 MW;
                                                                                                   Query Match
Best Local Similarity 60.0.
Best Local 9; Conservative
                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WKMKPRRNLEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WKMKSSENFEE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vitamin A; Transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIFFERENTIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9031;
                                                                                                                                                                                                                        RET4_CHICK
ID RET4_CHICK
AC P30370;
                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ERRATUM,
                                                                                                                                                                                                                                                                                                     CRABP2.
                                                                                                                                                                                                                                                                                                                                               Gallus
                                                                                                                                                                                                              RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
   SS THE SS
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RESULT 12

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MEDLINE=99146382; PubMed=10023777;

Novick D., Kim S.-H., Fantuzzi G., Reznikov L.L., Dinarello C.A.,

Rubinstein M.;
                                                                                                                                                                                                                                                                                                                          MEDLINE-95034308; PubMed-7947321;
Ho L., Mercola M., Gudas L.J.;
"Xenopus laevis cellular retinoic acid-binding protein: temporal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- FUNCTION: CYTOSOLIC CRABPS MAY REGULATE THE ACCESS OF RETINOIC ACID TO THE NUCLEAR RETINOIC ACID RECEPTORS.
-1- SUBCELLULAR LOCATION: Cytoplasmic.
-1- SIMILARITY: Belongs to the fatty-acid binding protein (FABP)
                                                                  01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Retinoic acid-binding protein, celluar (CRABP).
Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo Sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                       spatial expression pattern during early embryogenesis.".
Mech. Dev. 47:53-64(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2193DDE7B095EC4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           095998; 0055993; 006027; Q9UBRY; 005998; 0050993; 006027; Q9UBRY; 006027; 00607 (Rel. 39, Last sequence update) 10-007-2003 (Rel. 42, Last annotation update) Interleukin-18 binding protein precursor (IL-18BP).
137 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.5%; Score 40; DB 63.6%; Pred. No. 11; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; 151265; 151265.
HSSP; P29373; 1CBS.
InterPro; 1PR000463; Fatty acid BP.
InterPro; 1PR000566; Lipocln_cytFABP.
PEdm; PF00061; lipocalin; 1.
PRINTS; PR00178; FATTYACIDBP.
PROSITE; PS00214; FABP; 1.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ΒY
                                                  (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 AA; 15524 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; S74933; AAB32580.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 63.6%;
les 7; Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 WKMKPRRNLEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 WKMKQSENFEE 17
                                                                                                                                                                                                                              Kenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vitamin A; Transport
                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                     NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                            01-0CT-1996
01-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC OCC OCC OCC OX REP REP REP RAY
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphorylation
                                                                                                                                              PIR; F71258; F71258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
es 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ICP4 HSVMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  002362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
ICP4_HSVMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98332770; PubMed=9665876;
Praser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Chaperone protein htpG (Heat shock protein htpG) (High temperature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treponema pallidum.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 1019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: Molecular chaperone. Has ATPase activity (By
                                                                                                                                                                                                   Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  > T (IN REF. 2).
5B58244A98D1590A CRC64;
                                                                                                                                                                                                                                                                                                                                                                               (IN REF. 2).
                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                               ST; FALSE NEG.
                                                                                                                                                                                                                                                                                                         SIMILARITY)
                                                                                                                                                                                                                                                                                                                           SIMILARITY)
                                                                                                                                                                                                                                                                                                                                          (IN REF. 2)
(IN REF. 2)
                                                                                                                                                                                                                                                                                                                                        I -> F (IN REF.
F -> Y (IN REF.
KKI -> NKS (IN R.
Y -> C (IN REF.
V -> A (IN REF.
K -> I (IN REF.
A -> G (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              -> P (IN REF.
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                                                                                                                                                                                                                                                                                          PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 41;
2; Mismatches
InterPro; IPR000719; Prot kinase.
InterPro; IPR00877; Ser thr pkin_AS.
InterPro; IPR00299; Tudor.
Pfam; PF00069; pkinase; 1.
Pfam; PF00567; TUDOR; 1.
Prodom; PD000001; Prot_kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; FALSE PROSITE; PS00104; PROTEIN KINASE ATP; FALSE PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS50304; TUDOR; 1.
                                                                                                                                                                                                                                                     TNASE-LIKE. COILED COIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42;
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(BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 53.8 tes 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Nichols;
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HTPG OR TP0984.
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                                                                                                                                                                                                                  Coiled coil
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BINDING
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AD 0813949, DT 15-DEC, DT 28-EEB-
DE Chaperry
DE Chaper
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083949;
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Matches
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the Buropean Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Virology 189:657-667(1992).

-i- FUNCTIONA: THIS IE PROTEIN IS A MULTIFUNCTIONAL PROTEIN CAPABLE OF MGRATING TO THE NUCLEUS, BINDING TO DNA, TRANS-ACTIVATING OTHER VIRAL GENES, AND AUTOREGULATING ITS OWN SYNTHESIS. IT IS REQUIRED FOR THE SWITCH FROM IMMEDIATE-EARLY TO EARLY MODE OF GENE EXPRESSION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Nucleus of infected cells. PTM: A long stretch of serine residues may be a major site of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-92351564; PubMed-1322594;
Anderson A.S., Francesconi A., Morgan R.W.;
"Complete nucleotide sequence of the Marek's disease virus ICP4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47.1%; Score 40.5; DB 1; Length 639; 50.0%; Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marek's disease herpesvirus (strain GA) (MDHV).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Marek's disease-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20202-7002-7093 (Rel. 27, Created)
01-0cT-1993 (Rel. 27, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1415 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                     HSSP; P02829; 1AH8.
TCGR; PTOP844;
HAMAP: MF 00505; -; 1.
InterPro; IPR001594; ATPbind_ATPase.
InterPro; IPR001404; HSp90.
Pfam; PP02518; HATPase c; 1.
Pfam; PF02183; HSP90; 2.
                                                                                                                                                                                                                                       EMBL; AE001265; AAC65938.1; -.
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246 WK-RPKSELKEEDY 258
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Promission in transcriptions of the property o
         InterPro; IPR000719; Prot kinase.
InterPro; IPR002999; Tudor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                development.
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NP BIND
BINDING
SEQUENCE
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                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=21175748; PubMed=11279525;
Wang P.J., McCarrey J.R., Yang F., Page D.C.;
Wan abundance of X-linked genes expressed in spermatogonia.";
Nat. Genet. 27:422-426(2001).
-!- CAPALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-! TISSUE SPECIFICITY: Testis specific. Expressed only in male germ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae; Murinae, Mus.
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-!- SIMILARITY: Contains 1 Tudor domain.
                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL). (POTENTIAL). (POTENTIAL).
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InterPro; IPR005154; Glyco_hydro_67.
Pfam; PF03648; Glyco_hydro_67; TXJan degradation; Hydrolase; Glycosidase; Glycoprotein; Signal.
SIGNAL 1 POTENTIAL.
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(POTENTIAL).
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-!- SIMILARITY: BELONGS TO FAMILY 67 OF GLYCOSYL HYDROLASES.
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Pred. No. 34;
3; Mismatches 3; Indels
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Serine/threonine protein kinase 31 (EC 2.7.1.37).
                                                                                                                                                                                                                                                                                                                                                                             ALPHA-GLUCURONIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GLCNAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93424 MW;
                                                                                                                                                                                                                                     EMBL; Z68706; CAA92949.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53.8%;
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108 KLSPKLNLKEDGY 120
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238
321
353
586
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238
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CARBOHYD
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InterPro; IPR008191; Maternal_tudor.

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28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Serine/threonine protein kinase 31 (BC 2.7.1.37) (Serine/threonine-
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- TISSUE SPECIFICITY: Testis specific.
-!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
-!- SIMILARITY: Contains 1 Tudor domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang P.J., McCarrey J.R., Yang F., Page D.C.;
"An abundance of X-linked genes expressed in spermatogonia.";
Nat. Genet. 27:422-426 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cloning of a new protein kinase gene related to human testis
                                                                                                                                                                                                                                                                           Score 42; DB 1; Length 1018; Pred. No. 41; Mismatches 4; Indels
                                                                                                                                                                                                      1206284ED4E90816 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                TNASE-LIKE.
COILED COIL (POTENTIAL)
                                                                                                 PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR008191; Maternal_tudor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21175748; PubMed=11279525;
                                                                                                                                                                                                          115027 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 24-1019 FROM N.A.
                                                                                                                                                                                                                                                                       48.8%;
ilarity 53.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     646 WKLVEKSNLEESD 658
                                                                                                                                                                                                                                                                                                                                                                                                                 1 WKMKPRRNLEEDD 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein kinase NYD-SPK).
137
245
358
1018
725
738
                     105 245
298 358
711 1018
717 72<u>5</u>
738 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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RA KUNST F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Derriss R., Bourschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Brouillet S., Bruschi C.V., Candwell B., Capuano V., Carter N.M.,

RA Bristo C., Fujita M., Fujita Y., Fuma S., Galizzi A., Daniel R.A.,

RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,

RA Fritz C., Fujita M., Fujita Y., Harden J., Harwood C.R., Henaut A.,

RA Hilbert H., Holsappel S., Hosono S., Hallo M.F., Itaya M., Jones L.,

RA Hilbert H., Holsappel S., Hosono S., Hallo M.F., Itaya M., Jones L.,

RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,

RA Rieger M., Rivolta C., Rocha E., Roche B., Ros M., Sadaie Y.,

RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

RA Setiguchi M., Tamakoshi A., Tanaka T., Takahashi H., Takemaru K.,

RA Takeuchi M., Tamakoshi A., Tanaka T., Takahashi H., Takemaru K.,

RA Takeuchi M., Tamakoshi A., Tanaka T., Takahashi H., Takemaru S.,

RA Takeuchi M., Tamakoshi A., Tanaka T., Ratensenger T.,

RA Voshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,

RH "The complete genome sequence of the Gram-posttive bacterium Bacillus

RH "The Complete genome sequence of the Gram-posttive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 390:249-256(1997).
-!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall conversion of pyruvate to acetyl-CoA and CO(2). It contains
01-MAY-1991 (Rel. 18, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase
complex (EC 2.3.1.12) (E2) (S complex, 48 kDa subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caldwell R.M., Ferrari E.; "Sequence analysis of the mobA-ampS region of the Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                 Hemila H., Palva A., Paulin L., Arvidson S., Palva I.; "Secretory S complex of Bacillus subtilis: sequence analysis and identity to pyruvate dehydrogenase."; J. Bacteriol. 172:5052-5063 (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                      Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Winters P., Caldwell R., Enfield L., Ferrari E.;
"The amps.nprE (124 degrees-127 degrees) region of the subtilis 168 chromosome: sequencing of a 27 kb segment identification of several genes in the area."; Microbiology 142:3033-3037 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=168;
MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97124187; PubMed=8969500;
                                                                                                                                                                                                                                                                                                                  MEDLINE=90368558; PubMed=1697575;
                                                                                                                 PDHC OR ACEC OR BSU14600.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                 Bacillus subtilis
                                                                                                                                                                                                   NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosome."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=168;
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multiple copies of three enzymatic components: pyruvate dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and lipoamide dehydrogenase (E3) ensymptoments: Public dehydrogenase (E3) complex POSSESSES ALSO BRANCHED-CHAIN

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MEDLINE=9629777; Pubmdc=8654984;
MEDLINE=9629777; Bubmdc=8654984;
Margolles-Clark E., Saloheimo M., Siika-Aho M., Penttilae M.;
The alpha-glucuronidase-encoding gene of Trichoderma reesei.";
Gene 172:171-172(1996).
--- FINCTION: RELEASES 40-METHYLGLUCURONIC ACID FROM XYLAN.
--- CATALYTIC ACTIVITY: An alpha-D-glucuronoside + H(2)O = an alcohol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycolysis; Transferase; Acyltransferase; Lipoyl; Complete proteome.

INIT MET 0 BY SIMILARITY.

DOMAĪN 1 85 LIPOYL BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Alpha-glucuronidase precursor (EC 3.2.1.139) (Alpha-glucosiduronase)
                    CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-acetylddhydrolipoamide.
COFACTOR: Contains 1 covalently bound lipoyl cofactor.
SUBUNIT: Forms a 24-polypeptide structural core with octahedral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ·
0
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Bukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes;
                                                                                                                     symmetry.
-!- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
-!- SIMILARITY: Contains 1 lipoyl-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Length 441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
NCBL_TaxID=51453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6B44D47879D134DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       847 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E1/E3 BINDING.
LIPOYL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.8%; Score 42; DB 46.7%; Pred. No. 17; ive 3; Mismatches
2-OXOACID DEHYDROGENASE (BCDH) ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, 299111; CAB1333.1; -.
FRE, D66718; D36718.
HSSP, P11961, 2PDE.
Subtilist; BG10209; pdhc.
InterPro; IPR001078; 20xoacid_dh.
InterPro; IPR001089; Biotin lipoyl.
InterPro; IPR003016; E3 binding.
InterPro; IPR00316; E3 binding.
InterPro; IPR00316; Lipoyl_BS.
Pfam; PF00198; 2-oxoacid_dh; 1.
Pfam; PF00198; 2-oxoacid_dh; 1.
Pfam; PF00117; e3_binding; 1.
ProDom; PD001115; 20xoacid_dh; 1.
ProDom; PD001115; 20xoacid_dh; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             + D-glucuronate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47407 MW;
                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M57435; AAA62683.1; -. EMBL; AF012285; AAC24934.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 WKMKPRRNLEEDDYL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 WFVKPNDEVDEDDVL 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85
181
42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          441 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGUA TRIRE
099024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACT SITE
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Hiraoka Y.;
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SEQUENCE
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                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Bucopean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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X MEDLINE=21848401; PubMed=11859360;

A WOOD V. GWilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

A Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

A Collins M., Comnor R., Cronin A., Davis P., Feltwell T., Fraser A.,

Gothles M., Gonnor R., Hadnin N., Hadris D., Hidalgo U., Hodgson G.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

Monney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Jorex K., O'Nell S., Pearson D., Quail M.A., Rabbinowitsch E.,

Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

RA Weltens T., Walstreels E., Ribeger M., Schaefer M., Mmilehead S.,

RA Weltens I., Vanstreels E., Rieger M., Schaefer M., Mmeller-Auer S.,

RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                     HOMOSERINE LACTONE (ODHL), AN AUTOINDUCER MOLECULE WHICH BINDS TO
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99279565; PubMed=10348908; Ohmiya R., Kato C., Yamada H., Aiba H., Mizuno T.; "A fission yeast gene (prrl(+)) that encodes a response regulator implicated in oxidative stress response.";
                        J. Bacteriol. 179:3004-3012(1997).
-!- FUNCTION: REQUIRED FOR THE SYNTHESIS OF N-(3-OXODECANOYL)-L-
                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                               -!- SIMILARITY: Belongs to the autoinducer synthetase family.
                                                                                                                                                                                                                                                                                                                                                             Score 44; DB 1; Length 193;
Pred. No. 3.2,
4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transcription factor prr1 (Pombe response regulator 1).
                                                                                                                                                                                                                                                                                                                Quorum sensing; Autoinducer synthesis.
SEQUENCE 193 AA; 22127 MW; 238B760CD8701188 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIL SCHPO STANDARD; PRT; 539 AA. 014283; Q9UTX5; 16-OCT-2001 (Rel. 40, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) 10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                       PRINTS; PR01549; AUTOINDCRSYN,
ProDom; PD002752; Autoind synth; 1.
PROSITE; PS00949; AUTOINDUCERS SYNTH; 1.
oxodecanoyl) -L-homoserine lactone.";
                                                                                                                                                                                                                                           InterPro; IPR001690; Autoind synth. Pfam; PF00765; Autoind synth; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochem. 125:1061-1066(1999).
                                                                                                                                                                                                                                                                                                                                                                51.2%;
                                                                                                                                                                                                                                                                                                                                                                              42.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                       1 WKMKPRRNLEEDDY 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                    48
                                                                                                                                                                                                                            EMBL; U69677; AAC45212.1;
                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 42.9
1es 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        |::| | :|
WELKTNRGMETDEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRRI OR SPACEC9,14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRR1_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P., Sacquence G. Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Large-scale screening of intracellular protein localization in living fission yeast cells by the use of a GFP-fusion genomic DNA library."; Genes Cells 5:169-190(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: INVOLVED IN OXIDATIVE STRESS. TRANSCRIPTION FACTOR THAT ACTS UPON TRRI AND CT11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLUIAR LOCATION: Nuclear (Potential).
-!- SIMILARITY: In the N-terminal section; belongs to the HSF family.
-!- SIMILARITY: Contains 1 response regulatory domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00415; HSF; 1.
SMART; SM00448; REC; 1.
PROSITE; PS00434; HSF DOMAIN; 1.
PROSITE; PS00110; RESPONSE REGULATORY; 1.
Transcription regulation; Sensory transduction; Nuclear protein; DNA-binding; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ding D.-Q., Tomita Y., Yamamoto A., Chikashige Y., Haraguchi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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PHOSPHORYLATION (BY SIMILA
F3B4945C595B2871 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ą
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               441
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InterPro; IPR00232; HSF_DNA_bind.
InterPro; IPR002341; HSF_BTS.
InterPro; IPR001789; Response_reg.
Pfam; PR00447; HSF_DNA_bind; I
Pfam; PF00072; response_reg; IPRNNTS; PR00056; HSFDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=968 h90;
MEDLINE=20223868; Pubmed=10759889;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z99168; CAB16301.1; -.
EMBL; AB027943; BAA87247.1; -.
PIR; T39150; T39150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB041768; BAB16722.1; -.
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ODP_BACSU
TO 00P2_BACSU
STANDARD;

AC P2183;
DT 01-MAY-1991 (Rel. 18, Created)
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 224-413 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 364 WKRQPRILLVEDDEL 378
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                                                                                                                                                                                                                                                                                                              Nature 415:871-880(2002).
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Best Local Similarity 60.00
Best Local 9; Conservative
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NCBI_TaxID=55601;
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VANI_VAL
ID VANI_VAL
P74945;
                                                        SEQUENCE
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=88289400; PubMed=3041371;
Zhang J., Deutscher M.P.;
"Escherichia coli RVase D: sequencing of the rnd structural gene and purification of the overexpressed protein.";
Nucleic Acids Res. 16:6265-6278(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAID=KIZ / MG165;
STRAID=KIZ / MG165;
STRAID=KIZ / MG165;
Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Mau B., Shao Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampel G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.; "A 460-kb DNA sequence of the Escherichia coli K-12 genome
                                                                                            EMBL; AF186249; AAF17479.1; -.

EMBL; AC005053; AAC79150.1; ALT_INIT.

EMBL; AC0045053; AAAL5620.2; -.

EMBL; BC0014802; AAAL1802.1; -.

Genew; HGNC:11370; STEAP.

MIN; 604415; -.

GO; GO:0005911; C:integral to plasma membrane; TAS.

GO; GO:0015267; F:channel/pore class transporter activity; TAS.

TARANSMEM 71

TRANSMEM 119 139 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 86; DB 1; Length 339; 100.0%; Pred. No. 4.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             55443A170C870387 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-CCT-2001 (Rel. 40, Last annotation update)
Ribonuclease D (EC 3.1.26.3) (RNase D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 375 AA.
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POTENTIAL.
POTENTIAL.
POTENTIAL.
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MEDLINE-97251358; PubMed-9097040;
                                                                                                                                                                                                                                                                                                                                                                                                                             39851 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 WKMKPRRNLEEDDYL 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                         91
139
184
238
278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                             164
218
258
291
339 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RND OR B1804. Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                               TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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RAD_ECOLI
ID -MAD
DT 01-MAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGRFAMS; TIGR01388; rnd; 1.
Hydrolase; Nuclease; Exonuclease; tRNA processing; Complete proteome.
SEQUENCE 375 AA; 42734 MW; AC056D3883712BAE CRC64;
                                                                                                                                                                                                                                                                                                                                    MOI. Gen. Genet. 242:241-249(1994).
-!- FUNCTION: CLEAVES MULTIMERIC TRNA PRECURSOR AT THE SPACER REGION.
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
                                                                                                                                                                                                         Fulda M., Heinz B., Wolter F.P.;
Furthe fadlo gene of Escherichia coli K12 is located close to rnd at 39.6 min of the chromosomal map and is a new member of the AMP-binding protein family ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=NBIO / Serotype 01;
MEDLINE=97284506; PubMed=9139920;
Milton D.L., Hardman A., Camara M., Chhabra S.R., Bycroft B.W.,
Stewart G.S.A.B., Williams P.;
"Quorum sensing in Vibrio anguillarum: characterization of the vanI/vanR locus and identification of the autoinducer N-(3-
corresponding to the 40.1-50.0 min region on the linkage map."; DNA Res. 3:379-392(1996).
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Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Listonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.3%; Score 45; DB 1; Length 375; 63.6%; Pred. No. 4.4; ive 2; Mismatches 2; Indels
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Autoinducer synthesis protein vanI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphomonoester.
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InterPro; IPR002562; 3 5 exonuclease.

InterPro; IPR002121; HRDC.

InterPro; IPR006292; Ribonuclease D.

InterPro; IPR006292; Ribonuclease D.
                                                                                                                                                                                 MEDLINE=94150456; PubMed=8107670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE000274; AAC74874.1; -.
EMBL; D90823; BAA15599.1; -.
EMBL; D90824; BAA15608.1; -.
EMBL; D90825; BAA15613.1; -.
EMBL; X70994; CAAS0322.1; -.
PIR; S01223; NRECD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01612; 3.5 exonuclease; Pfam; PF00570; HRDC; 1.
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SMART; SM00341; HRDC; 1.
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Best Local Similarity 63.0
Tr Conservative
                                                                                                                    OF 1-38 FROM N.A.
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GenCore version 5.1.6
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OM protein - protein search, using sw model

July 12, 2004, 13:52:02 ; Search time 4.7093 Seconds (without alignments) 165.853 Million cell updates/sec Run on:

US-10-010-667A-2_COPY_14_28 86 1 WKMKPRRNLEEDDYL 15 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	0 0 0		Q9uhe8 homo sapien	esche	P74945 vibrio angu			trichoder	_		trepo	_		xenopns	3 homo sar						-	_	~				P12747 vibrio fisc		P75162 mycoplasma		bacil	Q00733 autographa		_	
SUMMARIES	TI.	- [STEA_HUMAN	RND_ECOLI	VANI VIBAN		ODP2_BACSU	AGUA_TRIRE	ST31 MOUSE		HTPG_TREPA			RET3_XENLA	118B_HUMAN	SYR_ARCFU	GPT1_CANAL	HTPG_FUSNN	VSN1_NOCAE	AKSF_METUA	IRF7 MOUSE	SLY1_DROME	SLY1_DROVI	YU20_DROME	DP27_CAEEL	OM22_HUMAN	LUXI_VIBFI	LEU3_LACLA	YG35_MYCPN	HAO1 HUMAN	ODP2_BACST	VP80_NPVAC	YGL4 YEAST	KEX1 YEAST	YBL7_YEAST
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	Score		98	45	44	43	42	42	42		40.5	40.5	40	40	40	40	-	39.5	65	39	39	39	39	33	6 C	B (n d	200	85	38	38	3.8	38	38	38
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P45182 haemophilus Q09820 schizosacch Q13563 homo sapien	Q02331 caenorhabdi P55200 mus musculu Q03164 homo sanien	018750 oryctolagus P08110 gallus gall P08113 mus musculu	P14625 homo sapien Q95m18 bos taurus P37363 pyrrhocoris
YDDB_HAEIN RNT1_SCHPO PKD2_HUMAN	YOL4_CABEL HRX_MOUSE HRX_HUMAN	ENPL_CHICK ENPL_CHICK ENPL_MOUSE	ENPL_HUMAN ENPL_BOVIN HEMI_PYRAP
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839 925 968	1371 3866 3969	716 795 802	803 804 133
44.2 44.2	4 4 4 4 4 4 5 2 5 4 4 5 5 5 5 5 5 5 5 5	43.6 43.6 6.6	43.6 43.6 43.0
8 8 8 8 8 8	3 B B	37.5 37.5 37.5	37.5 37.5 37
3 3 5 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	37 38 39	4 4 4 0 1 2	44 44 5

ALIGNMENTS

Search completed: July 12, 2004, 14:10:23 Job time: 24.1512 secs

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Activated protein kinase C receptor homolog.
Trypanosoma vivax.
Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
                                                                                                                                                                                                                                                                           Oryza sativa (Rice).
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=ILDatl.2;
Djikeng A., Majiwa P.A.;
"Trypanosoma vivax homologue of the receptor for activated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=cv. Nipponbare;
Sasaki I., Matsumoto I., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0406H10.";
Submitted (UUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AP002524; BAB07964.1;
Gramene; Q9LGG0;
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2058 AA; 226376 MW; 8A06B6562B8BBD69 CRC64;
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Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AFI00287, AAC73850.1;
GO; GO:0016301; F:kinase activity; IEA.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 7.
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Last annotation update)
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                         PRT; 2058 AA.
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01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2002 (TrEMBLrel. 22,
P0406810.14 protein.
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Best Local Similarity 50...
7; Conservative
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                                                                         PRELIMINARY;
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Best Local Similarity
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SEQUENCE FROM N.A.
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                                                                                                    Q9LGG0;
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STRAIN=Goel / Gol / ATCC BAA-199 / DSM 3647 / OCM 88;
STRAIN=Goel / Gol / ATCC BAA-199 / DSM 3647 / OCM 88;
MEDLINE=Z1220827; PubMed=12125824;
A Belline=Z-2120827; PubMed=12125824;
A Martinez-Arias R., Henne A., Martsch T., Merkl R., Schmitz R.A.,
Baneggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,
Brieggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,
Brieggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,
Brieggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,
Brieggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,
Brieggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,
Britz Britz H.-J., Gottschalk G.,
The genome of Methanosarcina mazei: evidence for lateral gene transfer between Bacteria and Archaea.",
J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
BEMBL; AE013238; AAM29858:1;
Britz-Pro; IPR004256; Drenard Arpase.
Britz-Pro; IPR004256; Drenard Arpase.
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                                                   "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; which comparison with genomes of Escherichia coli K12 and O157."; muclic Acids Res. 30.4432-4441 (2002).

BMBL; AE015166; AAM43025.1; GGC 60.005737; C:cytoplasm; IEA.

GO; GO:0005737; C:cytoplasm; IEA.

GO; GO:0008476; F:nucleic acid binding; IEA.

GO; GO:0004576; F:nucleic acid binding; IEA.

GO; GO:0004576; F:nucleic acid binding; IEA.

GO; GO:0004576; F:nucleic acid binding; IEA.

InterPro; IPR002562; 3; Exonuclease.

InterPro; IPR006292; Ribonuclease_D.
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Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y., Yu J.,
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Pred. No. 23;
4; Mismatches 2; Indels
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SEQUENCE 375 AA; 42762 MW; 49FA4111C3552E34 CRC64;
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Methanosarcina mazei (Methanosarcina frisia).
Archaea; Buryarchaeota; Buryarchaeota orders incertae
Methanosarcinales; Methanosarcinaceae; Methanosarcina.
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Last annotation update)
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Pfam; PF03008; DUF234; 1.
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MEDLINE=21074935; Pubmed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterchaemorrhagic Escherichia coli O157:H7.";
Nature 409:529-533(2001).
                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RND secons processes tRNA precursor.
RND OR Z2847 OR ECS2518
Escherichia coli 0157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Score 45; DB 16; Length 371;
Pred. No. 18;
                   2; Indels
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                    Mismatches
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SMART; SM00341; HRDC; 1.
    52.3%;
63.6%;
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                                                      338 WKLKPONNLPE 348
                                                                                                PRELIMINARY;
                                     1 WKMKPRRNLEE 11
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1 WKMKPRRNLEE 11 ||:||: || | 342 WKLKPQNNLPE 352

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REPORTINGE A. Burland V., Plunkett G.

REPORTINGE S. Burland V., Blattner R.R.;

REPORTINGE SCHETCHIS CONTROL S., Schwartz D.C., Perna N.T.,

REPORTINGE SCHETCHIS CONTROL CONTROL COMPLET G.

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MEDLINE=22272406; PubMed=1284590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Jin Q., Yang T., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun D., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Bacterichia; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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SEQUENCE 375 Aa; 42718 MW; 10A40D3DC7747AEA CRC64;
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01-UNN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
NAMSE D, processes tRNA precursor.
RND OR 251424.
                                                                         01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Ribonuclease D (EC 3.1.26.3).
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SMART; SM00341; HRDC; 1.
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Matches 7; Conservative
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PRELIMINARY;
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                                                                                                              Matches
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Matches
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Q9UTAS
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SEQUENCE FROM N.A.
SEQUENCE STRONGE STATE TO THE STATE STAT
                                                                              Gaps
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Bacteria: Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBI_TaxID=1351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leptospira interrogans.
Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
NCBI_TaxID=173;
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0
              DB 16; Length 243;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.7%; Score 47; DB 16; Length 475; 50.0%; Pred. No. 10; iive 4; Mismatches 3; Indels
                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ren S.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB011517; AAN50813.1; -.
InterPro; IPR006664; Bac OmpA.
InterPro; IPR0066665; OmpĀ/NotB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     475 AA; 55426 MW; 5394208BB7DC717B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22905 MW; 4050BD05B0CBDA98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
                                                                     3;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                          475 AA
  54.7%; Score 47; DB
40.0%; Pred. No. 5.2;
tive 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00691; OmpA; 1.
PRINTS; PR01021; OMPADOMAIN.
ProDom; PD000930; OmpA/MotB; 1.
                                                                                                                                                 ||::|::|:|
91 WKVRPQKKLDEDSVI 105
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                                                                                                              1 WKMKPRRNLEEDDYL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 299:2071-2074(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 WKLKPGENVELNEY 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 WKMKPRRNLEEDDY 14
                                                             6; Conservative
                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conserved domain protein.
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Query Match
Best Local Similarity
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SEQUENCE 208 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome. SEQUENCE 475 AA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                       Matches
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Q8F081
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                                                     Gaps
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Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL133225; CAB61781.1; -
PIR; TS0202; TS0202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=2457T / ATCC 700930 / Serotype 2a;
MEDIJNE=22590274; PubMed=12704152;
MEDIJNE=22590274; PubMed=12704152;
Mei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
Mau B., Perra N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
"Complete genome sequence and comparative genomics of Shigella
flexneri serotype 2a strain 2457T.";
Infect. Immun. 71:2775-2786 (2003).
EMBL, AB016983; AAP16920.1; --
SEQUENCE 371 AA; 42225 MW; 00577552B66FEA2D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shigella flexneri.
Bacteria; Protoobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
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    DB 16; Length 208;
                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UDN-2003 (TrEMBLrel. 24, Last annotation update)
Conserved hypothetical protein.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
  Score 46; DB 7
Pred. No. 6.6;
                                                                                                                                                                                                                                                  237 AA.
                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371 AA.
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InterPro; IPR003827; DUF207.
Pfam; PF02676; DUF207; 1.
53.5%;
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220 RMKPRRKLRNMDDYL 234
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01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                             :||:| ||| ||:
117 IKPKRYLEEGDYI 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 KMKPRRNLEE-DDYL 15
                                                                                    3 MKPRRNLEEDDYL 15
                                          8; Conservative
                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 66.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein. SEQUENCE 237 AA; 2
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NCBL_TaxID=4896;
                  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                   SPAC25B8.15C
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STEAP OR 2410007B19RIK.
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                                                                                                                    SEQUENCE FROM N.A.
                                                                     NCBI_TaxID=10090;
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Matches
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                                                                                                                                                                                            STRAIN=CS7BL/6;
MEDINDE=21371909; PubMed=11479226;
MEDINDE=21371909; PubMed=11479226;
Yang D., Holt G.E., Velders M.P., Kwon E.D., Kast W.M.;
Yang D., Holt G.E., Velders M.P., Kwon E.D., Kast W.M.;
stem cell antigen, and prostate-specific membrane antigen: prostate-specific cell-surface antigens highly expressed in prostate cancer of transgenic adenocarchoma mouse prostate mice.";
Cancer Res. 61:5857-5860 (2001).
EMBL; AF297098; AAK83126.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Serru V., Manivet P., Lamblin D., Vaubourdolle M., Kellermann O.,
Loric S.;
                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 63; DB 11; Length 339;
Pred. No. 0.011;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of human STEAP.";
Submitted (ARR-2011) to the EMBL/GenBank/DDBJ databases.
EMBL; AY020584; ARX50537.1; -.
MGD; MGI:1917608; Steap.
SEQUENCE 339 AA; 39109 MW; 32A2C29F2E333BD0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     339 AA; 39318 MW; 4B26A71FF559E84F CRC64;
        01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Six-transmembrane epithelial antigen of the prostate.
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:1917608; Steap.
GO; GO:0016021; C:integral to membrane; IEA.
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01-JUN-2001 (TrEMBLrel. 17,
01-OCT-2002 (TrEMBLrel. 22,
2410007B19Rik protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 73.3%;
Best Local Similarity 71.4%;
Matches 10; Conservative
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01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2003 (TrEMBLrel. 24,
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                                                                        Mus musculus (Mouse).
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                                                                                                                                                        [1]
SEQUENCE FROM N.A.
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XA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Arakawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

XA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

XA Aito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

XA Radota K., Matsuda H.A., Ashburner M., Baralov S., Casavant T.,

XA Radota K., Matsuda H.A., Ashburner M., Baralov S., Casavant T.,

XA Radota K., Matsuda H.A., Ashburner M., Baralov S., Casavant T.,

XA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

XA Sakai K., Okido T., Furuno M., Carninoi P., de Bonalo M.F.,

Blake J., Boile J., Holmann M., Hume D.A., Kamiya M., Lee N.H.,

A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

XA Myonshaw-Boris A., Yoshida K., Mashimad M., Rodriguez I., Sakamoto N.,

A Saaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

XA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

XA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

XA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

XA "Functional m.Dotation of a full-length mouse cDNA collection.";
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                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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NCBI_TaxID=670;
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Pred. No. 0.011;
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BMBL, AKOLO437; BABZ638.1, -.
MGD, MGI:1917608; Steap.
SEQUENCE 339 AA, 39264 MW, 3F7AB9C7520F0968 CRC64;
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Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Last sequence upd
01-OCT-2003 (TrEMBLrel. 25, Last annotation u
Putative DNA polymerase III, epsilon subunit.
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GO, GO:0005622; C:intracellular; IEA.
GO; GO:0004527; F:exonuclease activity; IEA.
InterPro; IPR066055; Exonuclease.
Pfan, PF00929; Exonuclease; 1.
Complete proteome.
SEQUENCE 243 AA; 27903 MW; 6696A2E2A0291
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Lancet 361:743-749(2003).
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Local Similarity 71.4%;
les 10; Conservative
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Mus musculus (Mouse).
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1017041 Total number of hits satisfying chosen parameters:

1017041 segs, 315518202 residues

Gapop 10.0 , Gapext 0.5

BLOSUM62

Scoring table:

Searched:

Sequence:

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

SPTREMBL 25:*

1: sp_archea:*
2: sp_bacteria:*
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ALIGNMENTS

SEQUENCE FROM N.A.

Nagasaka I., Boulday G., Coupel S., Coulon F., Tesson L.,
Heslan J.-M., Soulillou J.-P., Charreau B.;
"Differential gene expression in endochelial cells during TNF-alphaand LPS-mediated activation.",
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF319659; AAG33868.1; -. Gaps 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
Six transmembrane endothelial antigen of PABC.
Sus scrofa (Pig).
Bukaryota: Metazoa, Chordata, Craniata, Vertebrata; Eutheleostomi;
Mammalia: Eutheria; Cetartiodactyla; Suina; Suidae; Sus. ۲; Query Match 78.5%; Score 67.5; DB 6; Length 338; Best Local Similarity 86.7%; Pred. No. 0.0018; Matches 13; Conservative 1; Mismatches 0; Indels 3 Indels 338 AA; 39918 MW; ED490E86E067A32B CRC64; 338 AA. PRT; 1 WKMKPRRNLEEDDYL 15 14 WKMKPRKNL-EDDYL 27 PRELIMINARY; SEQUENCE Q9GL50 AC AC DIT DIT DIT DIT SERVENT à g

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Q924J9 PRELIMINARY; PRT; 339 AA. Q924J9; TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) RESULT 2 Q924J9 ID Q924J AC Q924Z DT 01-DE

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The invention describes a composition comprising a substance that modulates the status of a protein (1) of 340 or 283 amino acids, or of any of the 15 sequences of 259 amino acids, given in the specification, or a molecule that is modulated by the protein, where the status of the cell that expresses the protein is modulated. The compositions, proteins, polymucleotides and methods are useful for treating and detecting cancer. The STBAP-1-related proteins are useful for generating cancer vaccines. The polymucleotides are useful as tools for delineating, with greater precision, cytogenetic abnormalities in the chromosomal region that encodes STBAP-1 that may contribute to the malignant phenotype. This is the amino acid sequence of a variant of human six transmembrane
                                                                                                                                                                                                                                                                                                                                      STEAP-1; six transmembrane epithelial antigen of the prostate; cancer; cancer vaccine; delineation; cytogenetic abnormality; cytostatic;
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                                    ABU98390 standard; protein; 258 AA.
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Best Local Similarity
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N-PSDB; ACD02604.
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ABU98390

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Search completed: July 12, 2004, 14:07:23 Job time: 75.7209 secs

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ABU98393 standard; protein; 258

RESULT 14 ABU98393

Length 258;

100.0%; Score 192; DB 6; 100.0%; Pred. No. 3.9e-18;

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modulates the status of a protein (I) of 340 or 283 amino acids, or of any of the 15 sequences of 259 amino acids, given in the specification, or a molecule that is modulated by the protein, where the status of the cell that expresses the protein is modulated. The compositions, proteins, polynucleotides and methods are useful for treating and detecting cancer. The STEAP-1-related proteins are useful for generating cancer vaccines. The polynucleotides are useful for delineating, with greater procession, cytogenetic abnormalities in the chromosomal region that the amino acid sequence of a variant of human six transmembrane.
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                                                                                                                                                Sequence 258 AA;
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                                                                                                    STBAP-1; six transmembrane epithelial antigen of the prostate; cancer; cancer vaccine; delineation; cytogenetic abnormality; cytostatic;
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                                                                         Novel human gene STEAP-1 variant 11.
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                                                                                                                                                                                                                                                          06-SEP-2002; 2002WO-US028371.
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05-APR-2002; 2002US-0370387P
                                              (first entry)
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Best Local Similarity 100.
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N-PSDB; ACD02607.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 258 AA;
                                                                                                                                                                    Homo sapiens.
                                              31-JUL-2003
                                                                                                                                                                                                                              20-MAR-2003
               ABU98393;
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                                                                                                                                     vaccine.
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RESULT 15

The invention describes a composition comprising a substance that modulates the status of a protein (1) of 340 or 283 amino acids, or of any of the 15 sequences of 259 amino acids, given in the specification, or a molecule that its modulated by the protein, where the status of the cell that expresses the protein is modulated. The compositions, proteins polymucleotides and methods are useful for treating and detecting cancer. The polymucleotides are useful as tools for delineating cancer vaccines. The polymucleotides are useful as tools for delineating, with greater encodes STEAP-1 that may contribute to the malignant phenotype. This is the amino acid sequence of a variant of human six transmembrane

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Jakobovits A;

Challita-Eid PM,

Raitano AB,

Ge W,

Faris M,

WPI; 2003-313240/30. N-PSDB; ACD02601.

comprising a substance that modulates the status of protein, useful for treating and detecting cancer.

New composition comprising a substance that modulates the STEAP-1-related protein, useful for treating and detecting

Example 2; Fig 2E; 248pp; English.

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status of

Jakobovits

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06-SEP-2001; 2001US-0317840P.
05-APR-2002; 2002US-0370387P.
                                                                                                                                                                                                                                                         06-SEP-2002; 2002WO-US028371
                                                         WPI; 2003-313240/30.
                                           (AGEN-) AGENSYS INC
                                                                                                                                                                                                                                          WO2003022995-A2
                                                                                                                                       Sequence 258 AA;
                                                             N-PSDB; ACD02603
          WO2003022995-A2.
                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                     31-JUL-2003
                                                                                                                                                                                                                                                  20-MAR-2003
   Homo sapiens.
                 20-MAR-2003
                                                                                                                                                                                              ABU98424;
                                                  Faris M,
                                                                                                                                                                               RESULT 11
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The invention describes a composition comprising a substance that modulates the status of a protein (1) of 340 or 283 amino acids, or of any of the 15 sequences of 259 amino acids, given in the specification, or a molecule that is modulated by the protein, where the status of the cell that expresses the protein is modulated. The compositions, proteins, polymucleotides and methods are useful for treating and detecting cancer. The STEAP-1-related proteins are useful for generating cancer vaccines. The polymucleotides are useful for delineating, with greater precision, cytogenetic abnormalities in the chromosomal region that encodes STEAP-1 that may contribute to the malignant phenotype. This is the amino acid sequence of a variant of human six transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STEAP-1; six transmembrane epithelial antigen of the prostate; cancer; cancer vaccine; delineation; cytogenetic abnormality; cytostatic;
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                                                                                                          New composition comprising a substance that modulates the status o
STBAP-1-related protein, useful for treating and detecting cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 192; DB 6;
; Pred. No. 3.9e-18;
0; Mismatches 0;
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                                   Challita-Eid PM,
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2002US-0370387P.
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                                     Ge W, Raitano AB,
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N-PSDB; ACD02606.
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(AGEN-) AGENSYS INC.
                                                                               WPI; 2003-313240/30.
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Best Local Similarity
Matches 34; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 258 AA;
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05-APR-2002;
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                                           Faris M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STEAP-1; six transmembrane epithelial antigen of the prostate; cancer; cancer vaccine; delineation; cytogenetic abnormality; cytostatic;
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STEAP-1-related protein, useful for treating and detecting cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 192; DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 RESYRYKLINWAYQQVQQNKEDAWIEHDVWRMEI 218
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                                                                                                                                                      06-SEP-2002; 2002WO-US028371.
                                                                                                                                                                                             06-SEP-2001; 2001US-0317840P.
05-APR-2002; 2002US-0370387P.
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0

Gaps

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Indels

Length 258;

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Jakobovits A;

The invention describes a composition comprising a substance that

Example 2; Fig 2J; 248pp; English

STEAP-1; six transmembrane epithelial antigen of the prostate; cancer; cancer vaccine; delineation; cytogenetic abnormality; cytostatic;

Novel human gene STEAP-1 variant 13.

(first entry)

31-JUL-2003

ABU98395;

ABU98395 standard; protein; 258 AA.

ABU98395

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                                                                            Gaps
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0
                                                Length 255;
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                                                                           Indels
                                         100.0%; Score 192; DB 6; 100.0%; Pred. No. 3.9e-18;
                                                                                                              185 RRSXRXKLLNWAYQQVQQNKEDAWIEHDVWRMEI 218
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                                                                                            1 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI
                                                   100.0%; Preu. ...
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                                                                    Conservative
                                                   Similarity
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             Sequence 255 AA;
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                                    Query Match
Best Local Simi
Matches 34;
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So
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Jakobovits A;

Challita-Eid PM,

Raitano AB,

Ge ₩

Faris M,

(AGEN-) AGENSYS INC.

WPI; 2003-313240/30. N-PSDB; ACD02609.

06-SEP-2002; 2002WO-US028371. 06-SEP-2001; 2001US-0317840P. 05-APR-2002; 2002US-0370387P.

WO2003022995-A2.

20-MAR-2003

Homo sapiens.

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The invention describes a composition comprising a substance that modulates the status of a protein (I) of 340 or 283 amino acids, or of any of the 15 sequences of 259 amino acids, given in the specification, or a molecule that is modulated by the protein, where the status of the polymucleotides and methods are useful for treating and detecting cancer. The STEAP-1-related protein is modulated. The compositions, proteins, The polymucleotides are useful for generating and detecting cancer. The polymucleotides are useful as tools for delineating, with greater procession, cytogenetic abnormalities in the chromosomal region that encodes STEAP-1 that may contribute to the malignant phenotype. This is the amino acid sequence of a variant of human six transmembrane
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cancer vaccine; delineation; cytogenetic abnormality; cytostatic;
vaccine.
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1 Similarity 100.0%; Pred. No. 3.9e-18;
34; Conservative 0; Mismatches 0.
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Matches
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218

Length 255;

100.0%; Score 192; DB 6; 100.0%; Pred. No. 3.9e-18; ive 0; Mismatches 0;

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1 RRSYRYKLLINWAYQQVQQNKEDAWIEHDVWRMEI 34

185 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI

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US-09-252-991A-31334
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NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                        Sequence 31334, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 54, Application US/09247373B
Patent No. 6168954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best
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LENGTH: 22:
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                                             PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31334
LENGTH: 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEFE, DANIEL
TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1108-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/247,373B CURRENT FILING DATE: 1999-02-10
                                                                                                                                                     FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                                                                                                      APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
SOFTWARE: Microsoft (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 08/924,747
PRIOR FILING DATE: 1997-09-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: SIGNAL LOCATION: (1)..(28)
                                                                                                                                    PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: SOYBEAN
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                ORGANISM: Pseudomonas aeruginosa
                                  TYPE: PRT
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nes 8; Conserv
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46.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40; DB Pred. No. 41; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 221;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Xaa = Asp, Tyr
US-09-621-976-5168
                                                                                                                  ; TYPE: PRT; ORGANISM: Vibrio fischeri
US-09-582-379-4
                                                                                                                                                                                                                                                                                                                                                            US-09-582-379-4
                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/621,976
CUBRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 5168
LEXECUTE: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Jobert, S.
APPLICANT: GLOCATION, J.Y.
TITLE OF INVENTION: ESTs and Encoded FILE REFERENCE: GENSET.054PR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5168, Application US/09621976 Patent No. 6639063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hest Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09582379 Patent No. 6492176 GENERAL INFORMATION:
                                                                                                                                                              SEQ ID NO 4
LENGTH: 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                     Query Match
Best Local 9
                                                          Matches
                                                                                                                                                                                        FILE REFERENCE: 001252
CURRENT APPLICATION NUMBER: US/09/582,379
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                  APPLICANT: K.U. Leuven Research & Development
TITLE OF INVENTION: Increase of No. 6492176ule number and nitrogen fixation in
TITLE OF INVENTION: leguminosae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 103
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                       27
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35
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7; Conserva
                                                         l Similarity
6; Conserv
                           1 WKMKPRRNIEEDDY 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   KPRRNLEEDD 13
   WDLVVENNLESDEY 48
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                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.2%;
                                                                        44.2%;
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Pred. No. 1.2e+02;
1; Mismatches 2;
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Pred. No.
                                                                          Score 38; DB 4; Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39;
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                                                                                        Length 193;
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US-08-403-866-2; Sequence 2; Ar

Application US/08403866

RESULT 11

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PRIOR APPLICATION NUMBER: US 60,
PRIOR FILING DATE: 1998-02-18
PRIOR PRICATION NUMBER: US 60,
PRIOR ETLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29449
LENGTH: 464
                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
US-09-22-991A-29449
S-09-252-991A-29449
Sequence 29449, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
US-09-252-991A-29449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-403-866-2
                                                                                                                                                                                                                                      TITLE OF INVENTION: NUCLEIC ACLD AND FUNCTIONS TO INVENTION: ABRUGINOSA FOR DIAGNOS FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
CURRENT FILING DATE: US/60/074,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Ehrlich,
APPLICANT: Godon, J
APPLICANT: Renault,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
              OTHER INFORMATION: Identity of amino acid
                                   NAME/KEY: UNSURE
LOCATION: (227), (276)
                                                                                          TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 2:
                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: PI
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 345 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPUTED:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Nucleic acid of TITLE OF INVENTION: synthase from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (716) 263-1600
TELEFAX: (716) 263-1487
TELEX: 978450 (WUT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 30, 727
REFERENCE/DOCKET NUMBER: 20747/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Goldman, Michael L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 KLSPIRNVENVDFL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 KMKPRRNLEEDDYL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                           Marc J. Rubenfield et al.

VENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS VENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      345 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Renault, Pierre
WENTION: Nucleic acid coding for an alpha-acetolactate
WENTION: synthase from Lactococcus and its applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ehrlich, Stammer Godon, Jean-Jacques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lactococcus lactis subsp. lactis ISOLATE: LEUB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
                                                                                                                                                                                           UMBER: US 60/094,190
1998-07-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38; DB 1;
Pred. No. 1.4e+02;
3; Mismatches 4
              at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 345;
          above locations are unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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Query Match

44.2%;

Score 38;

DB

4;

Length 464;

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Query Match
Best Local Similarity 4.
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US-09-107-532A-6422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT ; ORGANISM: Enterococcus faecalis US-09-134-000C-4765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
US-09-134-000C-4765
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 4765
LENCTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6422, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4765, Application US/09134000C Patent No. 6617156
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/134,000C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/055,778 PRIOR FILING DATE: 1997-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: ENTERCOCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 032796-032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH:
                                                  APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/081571
FILING DATE: July 2, 1997
ATTORNEY/AGBUT INFORMATION:
NAME: Ariniello, Pamela Deneke
                                                                                                                                                                                                                       OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                              ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/RO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 WFVKPGDTINEDDTL 37
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             NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                        CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                 COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
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46.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7310
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Pred. No. 2.4e+02;
2; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FABCIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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RESULT 15
US-08-651-999A-7
(Sequence 7, Application US/08651999A
Patent No. 6031088
GENERAL INFORMATION:
APPLICANT: Stefan Somlo and Toshi
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                                                                                                                                                                                                  COMPUTER: INM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/651,999A
PILING DATE: MAY 23, 1996
ATTORNEY/ASENT INFORMATION:
NAME: ELIZABETH A. BOGOSIAN
REGISTRATION NUMBER: 96700/395
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 2697-5995
TELIEFAX: (212) 2697-5995
TELIEFAX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 968 amino acids
TYPE: amino acid
STEADDENMESS: sincle
                                                                                     US-08-651-999A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 44.2%; Score 38; DB 4; Length 555; Best Local Similarity 46.7%; Pred. No. 2.4e+02; Matches 7; Conservative 2; Mismatches 6; Indels
Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6422:
SEQUENCE CHARACTERISTICS:
                                                                                                  MOLECULE TYPE:
DESCRIPTION:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE
MEDIUM TYPE: DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Stefan Somlo and Toshio Mochizuki
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE PKD2 GENE
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
ZIP: 10016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN
STREET: 90 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                 STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...555
SEQUENCE DESCRIPTION: SEQ ID NO: 6422:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 WKMKPRRNLEEDDYL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 555 amino acids
    Conservative
                                                                                                      : peptide
NO
                     44.2%; Score 38; DB 3; Length 968; 46.2%; Pred. No. 4.5e+02;
  2; Mismatches
    5
      Indels
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    0;
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    Gaps
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Title:
Perfect
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Maximum
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                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                Database
                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                       Searched:
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DB
                                                                                                                                                                                                                                                                                                                                                                                                  score:
                                                                                                                                                                                                                          seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein search, using sw model
   A_Geneseq_29Jan04:*
1: geneseqp1990s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003bs:*
7: geneseqp2003bs:*
                                                                                                                                                                                                                          length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                July 12, 2004, 13:51:07; Search time 32.9651 Seconds (without alignments)
128.567 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                  US-10-010-667A-2_COPY_14_28
86
                                                                                                                                                                                                                                                                                                       1586107 segs, 282547505 residues
                                                                                                                                                                                                                                                                                                                                    Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                     WKMKPRRNLEEDDYL 15
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geneseqD2002s:*
geneseqD2003as:*
geneseqD2003bs:*
geneseqD2004s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 5.1.6 (c) 1993 - 2004 Compus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Synthetic.

recombinant protein.

25	24	23	22	21	20	19	18	17	16			13	12	11	10	9	8	7	თ	υ	4	ω	2	ц	Result
86	86	86	86	86	86	86	86	86	96	86	86	96	86	86	86	86	86	86	86	86	96	86	86	96	Score
100.0	100.0	100.0	100.0		100.0	100.0	100.0	100.0		100.0			•	100.0	•	•			•	100.0	•	•	100.0	100.0	Query Match
258	258	258	258	258	258	258	258	258	258	258	258	258	258	258	258	258	255	255	254	254	109	- 66	15	15	Length 1
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ABU98398	ABU98399	ABU98386	ABU98388	ABU98394	ABU98397	ABU98396	ABU98431	ABU98384	ABU98391	ABU98390	ABU98393	ABU98387	ABU98392	ABU98424	ABU98389	ABU98395	ABU98428	ABU98429	ABU98425	ABU98426	AAY12304	AAY12305	AAE02784	AAY58201	ID
Abuy8398 Novel Hum	Novel	Novel	Novel	Novel	Novel	Novel	STEAP-	Novel	Novel	Novel	Novel	Abu98387 Novel hum	Novel	STEAP-		Novel	8 STEAP-	STEAP-	u		4	Human 5	4 Immuno		Description

45	44	43	42	41	40	39	38	37	36	35	34	ယ္	32	31	30	29	28	27	26
70	86	86	86	86	98	86	86	86	86	98	96	86	86	86	86	86	86	86	96
81.4	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
95	375	374	339	339	339	339	339	339	339	339	339	339	339	339	339	339	282	282	282
N	4,	4	7	7	7	g	σ	δ	σ	U	σı	4	4.	4	4	w	σ	თ	თ
AAY11840	AAE02780	AAM79829	ADB14329	ADB75573	ABU63313	ABR54499	ABU98430	ABU98414	ABU98383	ABG61813	ABB95387	ABU71818	AAM78845	AAU69927	AAM01282	AAY58194	ABU98385	ABU98427	ABU98432
Aayii840 Human 5	Human	Human	Human	Prosta	-	_						-		Human	768/4	Human	TOVET	STEAP	

Human STRAP-1 peptide 1, corresponding to STRAP-1 residues 14-28. 14-MAR-2000 AAY58201; AAY58201 standard; peptide; 15 (first entry) AA.

ALIGNMENTS

Serpentine transmembrane antigen of the prostate; STRAP-1; prostate; transmembrane domain; type IIIa membrane protein; expression; cancer; prostate cancer; bladder cancer; colon cancer; panoreatic cancer; ovarian cancer; tumour antigen; immunisation; immune response; cellular; ovarian cancer; vaccine; antibody; detection; diagnosts; prognosts; humoral; anticancer vaccine; antibody; detection; diagnosts; prognosts; monitoring; susceptibility; therapeutic inhibitor; drug targetting;

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(UROG-)
                                                                        01-JUN-1998;
30-JUN-1998;
                                                                                    01-JUN-1999;
                                                                                            09-DEC-1999
                                                                                                   WO9962941-A2
                                                                                                           Homo sapiens.
                              WPI; 2000-072832/06.
                                      Afar DE,
                                             (RAIT/)
(SAFF/)
                                                         (HUBE/)
                                                     (LEON/)
                                             LEONG K.
RAITANO A B.
SAFFRAN D C.
                                                         AFAR D E.
HUBERT R S.
                                                                 UROGENESYS INC.
                                      Hubert RS,
                                                                         98US-0091183P
                                                                            98US-0087520P
                                                                                    99WO-US012157.
                                      Leong
                                      ×
                                      Raitano AB,
                                       Saffran
                                       DC;
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Novel proteins useful as diagnostic markers and therapeutic targets, particularly for prostatic cancer.

Example 3C; Page 41; 83pp; English.

This sequence represents a synthetic peptide (peptide 1) corresponding residues 14-28 of STRAP-1 (serpentine transmembrane antigen of the to

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CC prostate, AAY58194). This peptide was used to raise polyclonal anti-STRAP CC Western blots of cell lysates from prostate and non-prostate cancer cell lines, and in immunohistochemical analysis of STRAP-1 expression. STRAP-1 cyc which exhibit a high degree of the STRAP family of proteins (AAY58194-Y58197) CC which exhibit a high degree of structural conservation, but which show no cell has been localised to chromosome 7p22. STRAP-1 is a 339 amino acid protein characterised by six transmembrane domains and intracellular N- and chermini, suggesting that it folds in a "serpentine" manner into three extracellular and two intracellular loops. STRAP-1 man and protein concernation but recein cancers. STRAP-1 man and characterised by six transmembrane domains and intracellular N- and chermini, suggesting that it folds in a "serpentine" manner into three expression is maintained at high levels and throughout all stages of certain other cancers, including bladder, colon, pancreatic and ovarian channels (from the presence of six transmembrane domains, a feature which is human strochemical staining). STRAP proteins is not known. They may be ion channels (from the presence of six transmembrane domains, a feature which is shared by certain ion channels) or gap-junction proteins (from the manner into three cell-surface and throughout all stages of concern immune responses against STRAP-expressing cells. STRAP proteins and concern cell-surface and concern capture that stransmembrane domains, a feature which is humoral immune responses against STRAP-expressing cells. STRAP proteins and concern cell-surface and concern capture responses against STRAP-expressing cells. STRAP proteins concern cell-surface and concern capture that stransmembrane domains, a feature which is shared by certain such stransmembrane domains, as STRAP proteins concern cell-surface and concern capture that stransmembrane domains cells. STRAP proteins concern cell-surface and concern capture stransmembrane domains, as feature which capture stransmembrane 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local :
                                                                         06-DEC-1999;
                                                                                                                   06-DEC-2000; 2000WO-US033040.
                                                                                                                                                                               07-JUN-2001
                                                                                                                                                                                                                           WO200140276-A2
                                                                                                                                                                                                                                                                                                                                      six transmembrane epithelial antigen of the prostate-1; STEAP-1; chromosome 7p22.3; cancer; prostate; colon; bladder; pancreatic; ovarian;
                       (UROG-) UROGENESYS INC
                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                     Human; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE02784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE02784 standard; peptide; 15 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-AUG-2001
                                                                                                                                                                                                                                                                                                                         lung; serpentine transmembrane antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunogenic peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 WKMKPRRNLEEDDYL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                           99US-00455486
                                                                                                                                                                                                                                                                                                                                                                                           antiproliferative; vaccine; gene therapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                               #1 of human STEAP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 86;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 8.3e-08;
                                                                                                                                                                                                                                                                                                                       immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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Д Ś 8888888888888888888888888888888888888

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AAX12305
ID AAX1
XX
AC AAX1
DY 17-C
XX
Huma
KW Huma
KW Lore
KW Lore
KW Lore
KW repi
KW 101-1
XX
DP 11-1
XX
DP 31-1
XX
DP 31-1
XX
DP 31-1
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DR 01-1
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DR 01-1
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DR 01-1
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DR WPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC The present invention relates to human six transmembrane epithelial CC antigen of the prostate (STEAP) protein. STEAP gene is used in gene CC therapy. Inhibiting the development or progression of a cancer (eg. CC prostate, colon, bladder, lung, ovarian and pancreatic) expressing STEAP (CC or inhibiting growth or killing cells expressing STEAP in a patient. Treating a vertice that expresses STEAP, or inhibiting growth or comprises administering a vertice composition to the patient. Treating a vertice that expresses STEAP, or inhibiting growth or CC killing cells expressing STEAP, comprises administering to the patient a vector encoding single chain monoclonal antibody that comprises the CC that specifically binds to STEAP, such that the vector delivers the CC that specifically binds to STEAP, such that the vector delivers the CC single chain monoclonal antibody is expressed contracellularly. The present sequence is an immunogenic paptide of STEAP-1 gene is located on chromosome 7p22.3. This peptide is used to communise sheep for the generation of sheep polyclonal antibodies towards the amino-terminus of anti-STEAP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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WPI; 1999-153778/13
                                Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                       Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostat
                                                                                                       01-AUG-1997;
                                                                                                                                      31-JUL-1998;
                                                                                                                                                                          11-FEB-1999
                                                                                                                                                                                                           WO9906548-A2
                                                                                                                                                                                                                                             Homo sapiens
                                                                    (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                Human 5' EST secreted protein SEQ ID NO:336
                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY12305
                                                                                                                                                                                                                                                                                thrombolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY12305 standard; protein; 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New STEAP (six transmembrane proteins, expressed in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3C; Page 77; 187pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-367804/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Faris M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Afar DEH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 WKMKPRRNLEEDDYL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                            anti-inflammatory; tumour inhibition.
                                                                                                     97US-00905135
                                                                                                                                        98WO-IB001222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 86; 100.0%; Pred. No.
                              Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Raitano AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   epithelial antigen of the prostate) cancers, useful for detecting and treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                              Lacroix B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saffran DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitchell SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                           haemostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   libraries
umbilical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                            differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY12304 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX41094 to AAX41347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acids encoding human secreted proteins - obtained from cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human 5' EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY12304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide into a membrane, or importing a polypeptide into a cell
New nucleic acids e
libraries prepared
                                                                                                                                                                                                                01-AUG-1997;
                                                                                                                                                                                                                                                        31-JUL-1998;
                                                                                                                                                                                                                                                                                                    11-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            forensic; gene therapy; chromosome mapping; signal peptide;
upstream regulatory sequence; cytokine activity; cell proliferation;
                                                                                                                              Dumas Milne Edwards
                                                                                                                                                                        (GEST )
                                                                                                                                                                                                                                                                                                                                            WO9906548-A2
                                                                                                                                                                                                                                                                                                                                                                                      Homo
                                                                                      1999-153778/13
                                                                                                                                                                                                                                                                                                                                                                                    sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        secreted protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                AAX41137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WKMKPRRNLEEDDYL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WKMKPRRNLEEDDYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prepared from e.g. liver, ovary, cord, placenta and colon tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 677-678; 824pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              secreted protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                  97US-00905135
                                                                                                                                                                                                                                                          98WO-IB001222
  encoding human
d from e.g. live
                                                                                                                              'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 represent
                                                                                                                                Duclert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST; expressed sequence tag; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
    iman secreted proteins -
liver, ovary, brain, pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 86;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO:335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
.... No. 4e-07;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ςį
                                                                                                                              P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expressed sequence tags
                                                                                                                                Lacroix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    brain, prostate, kidney, lung,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                          obtained from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ags (ESTs) for in AAY12261 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                        CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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prostate,

kidney,

The invention describes a composition comprising a substance that modulates the status of a protein (1 of 340 or 283 amino acids, or of any of the 15 sequences of 259 amino acids, given in the specification, or a molecule that is modulated by the protein, where the status of the

Example

53

Page 169-170;

248pp; English.

protein,

treating

and

detecting

cancer

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RESULT 5
ABU98426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequences can be used for products for diagnosis and therapy. The proliferation/differentiation activity, cell proliferation/differentiation activity, haematopoiesis regulating activity, tissue growth regulating activity, reproductive hormone regulating activity, chemotactic/ chemokinetic activity, haematopy activity, haematopy and thrombolytic activity, receptor/ ligand activity, anti-inflammatory activity, tunour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The mucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human secreted proteins, and encode the proteins given in AAY12261 AAY12514, respectively. The proteins given represent the signal pepand an N-terminal fragment of a secreted protein. The nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 umbilical
                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                             vaccine.
                                                                                                                                                                                                                                                                                                                                         STEAP-1; six transmembrane epithelial antigen of the prostate; cancer; cancer vaccine; delineation; cytogenetic abnormality; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                             STEAP-1 variant 8P1D4 v.2
                                                                                                                                                                                                                                                                                                                                                                                                     31-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                             ABU98426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU98426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX41094 to AAX41347 represent 5'
                                                                                                                                                                                        06-SEP-2001;
05-APR-2002;
                                                                                New composition STEAP-1-related
                                                                                                                                            Faris
                                                                                                                                                                                                                             06-SEP-2002; 2002WO-US028371.
                                                                                                                                                                                                                                                      20-MAR-2003
                                                                                                                                                                   (AGEN-) AGENSYS INC.
                                                                                                                     2003-313240/30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 WKMKPRRNLEEDDYL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WKMKPRRNLEEDDYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 677; 824pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cord, placenta and colon
                                                                                                                                            Ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                           Σ
                                                                                                                                                                                           2001US-0317840P.
2002US-0370387P.
                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                  comprising a substance protein, useful for tr
                                                                                                                                            Raitano
                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
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                                                                                                                                             ΑB,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     254
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Pred.
                                                                                                                                             Challita-Eid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expressed sequence tags (ESTs) for the proteins given in AAY12261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue
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                                                                                                that
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                                                                                                                                             PM,
                                                                                                modulates
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                                                                                                                                             Jakobovits
                                                                                                the status
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RESULT 6
ABU98425
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ID 98425
ID 98425
ID 98425
ID 31-J
XX ABU9
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XX STEA
XX Canc
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XX ION
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XX WO20
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PM WP1;
IN FARI
XX WP1;
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XX INEW
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Best Local Similarity
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                                                                                                                                                 The invention describes a composition comprising a substance that modulates the status of a protein (I) of 340 or 283 amino acids, or of any of the 15 sequences of 259 amino acids, given in the specification, or a molecule that is modulated by the protein, where the status of the cell that expresses the protein is modulated. The compositions, proteins, polymucleotides and methods are useful for treating and detecting cancer. The STEAP-1-related proteins are useful for generating cancer vaccines. The polymucleotides are useful as tools for delineating, with greater precision, cytogenetic abnormalities in the chromosomal region that encodes STEAP-1 that may contribute to the malignant phenotype. This is the amino acid sequence of a variant of human six transmembrane epithelial antigen of the prostate or STEAP-1
                                                                                                        Sequence 254 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New composition comprising a substance that modulates the status of a STEAP-1-related protein, useful for treating and detecting cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-SEP-2001; 2001US-0317840P.
05-APR-2002; 2002US-0370387P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell that expresses the protein is modulated. The compositions, proteins, polymucleotides and methods are useful for treating and detecting cancer. The STRAP-1-related proteins are useful for generating cancer vaccines. The polymucleotides are useful as tools for delineating, with greater precision, cytogenetic abnormalities in the chromosomal region that encodes STEAP-1 that may contribute to the malignant phenotype. This is the amino acid sequence of a variant of human six transmembrane epithelial antigen of the prostate or STEAP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-313240/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Faris M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STEAP-1; six transmembrane epithelial antigen of the prostate; cancer; cancer vaccine; delineation; cytogenetic abnormality; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STEAP-1 variant 8P1D4 v.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AGEN-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-SEP-2002; 2002WO-US028371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 254 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 WKMKPRRNIEEDDYL 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 WKMKPRRNLEEDDYL 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53; Page 169-170; 248pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGENSYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ge ₩,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Raitano AB,
      100.0%;
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      Score
Pred.
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Pred. No. 1.7e-06;
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No.
   DB 6;
1.7e-06;
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                                     Length 254;
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ABU98428 ID ABUS

ABU98428 standard;

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ABU98428

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RESULT 7
ABU98429
ID ABU98429
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                                                                                                            Query Match
Best Local S
Matches 15
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                                                                                                                                                                                                                                                                           The STEAP-1-related proteins are useful for generating cancer vaccines. The polynucleotides are useful as tools for delineating, with greater precision, cytogenetic abnormalities in the chromosomal region that encodes STEAP-1 that may contribute to the malignant phenotype. This is the amino acid sequence of a variant of human six transmembrane epithelial antigen of the prostate or STEAP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes a composition comprising a substance that modulates the status of a protein (I) of 340 or 283 amino acids, or of any of the 15 sequences of 259 amino acids, given in the specification, or a molecule that is modulated by the protein, where the status of the cell that expresses the protein is modulated. The compositions, proteins, polynncleotides and methods are useful for treating and detecting cancer.
                                                                                                                                                                                                                            Sequence 255 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 53; Page 172; 248pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New composition comprising a substance that modulates the status STEAP-1-related protein, useful for treating and detecting cancer
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05-APR-2002; 2002US-0370387P.
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                                                       1 WKMKPRRNLEEDDYL 15
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                                                                                                                                          Similarity
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                                                                                                               Conservative
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28
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                                                                                                                                       Score 86;
Pred. No.
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                                                                                                                                          1.7e~06;
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                                                                                                                                                              Length 255;
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RESULT 9
ABU9839
ID ABU99
XX ABU99
XX ABU99
XX ABU9
XX ABU9
XX NOVe
XX NOVe
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XW CANC
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Best Local 9
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                                                                                                                                                                             STEAP-1; six tracancer vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New composition STEAP-1-related
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05-APR-2002; 2002US-0370387P.
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                                                                                                                                                                                                                                                           Novel human gene STEAP-1 variant 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 255
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                                                                                                                                                          vaccine.
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                                                                                                                                                                                                                                                                                                                                                                ABU98395;
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     20-MAR-2003
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                                                                                                     sapiens
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15; Conserv
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                                                                                                                                                                                                     six transmembrane
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                                                                                                                                                                                  delineation;
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                                                                                                                                                                                                        epithelial
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Pred. No. 1.7
D; Mismatches
                                                                                                                                                                             withelial antigen of the prostate; cytogenetic abnormality; cytostat
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1.7e-06;
0;
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                                                                                                                                                                                cytostatic;
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RESULT 10
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ID ABU98389
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XX ABU98
XX STEAF
KW CAINCE
KW CAINCE
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05-APR-2002; 2002US-0370387P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 258 AA;
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05-APR-2002; 2002US-0370387P
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                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STEAP-1; six transmembrane epithelial antigen of the prostate; cancer; cancer vaccine; delineation; cytogenetic abnormality; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABU98389;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ACD02609.
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        N-PSDB; ACD02603
                              WPI; 2003-313240/30
                                                                               Faris M,
                                                                                                                                                                                                                                                                                                                            20-MAR-2003.
                                                                                                                                    (AGEN-)
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B
                                                                               Ge W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2M; 248pp; English
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                                                                                     Raitano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STEAP-1 variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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                                                                                     ₽В,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 86;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Challita-Eid PM,
                                                                                     Challita-Eid PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.
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                                                                                     Jakobovits
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RESULT 11
ABU98424
ID 38424
ID 38424
ID 38424
AC ABU98
XX ABU98
XX STEAP
XX STEAP
XX WC220(
XX WC220(
XX WC220
PP 06-SI
PR 05-AI
XX PF 06-SI
PR 05-AI
YX AGEI
PR 05-AI
YX AGEI
PR 05-AI
YX AGEI
PR 05-AI
YX AGEI
PR 06-SI
XX AGEI
PR 06-SI
XX INGEN
PR 15-AI
YX AGEI
PR 15-AI
YX AGEI
PR 17-AI
PT STEAP
XX PTEA
XX AGEI
PT STEAP
XX CC The
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Matches
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               The invention describes a composition comprising a substance that modulates the status of a protein (I) of 340 or 283 amino acids, or of any of the 15 sequences of 259 amino acids, given in the specification, or a molecule that is modulated by the protein, where the status of the cell that expresses the protein is modulated. The compositions, proteins, polynucleotides and methods are useful for treating and detecting cancer.
                                                                                                                                                                                                         New composition comprising a substance that modulates the status of STEAP-1-related protein, useful for treating and detecting cancer.
      polynucleotides and
The STEAP-1-related
                                                                                                                                                                                                                                                                              WPI; 2003-313240/30.
                                                                                                                                                                                                                                                                                                                       Faris M,
                                                                                                                                                                                                                                                                                                                                                                                                 06-SEP-2001; 2001US-0317840P
05-APR-2002; 2002US-0370387P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STEAP-1; six transmembrane epithelial antigen of the prostate; cancer; cancer vaccine; delineation; cytogenetic abnormality; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The STEAP-1-related proteins are useful for generating cancer vaccines. The polymucleotides are useful as tools for delineating, with greater precision, cytogenetic abnormalities in the chromosomal region that encodes STEAP-1 that may contribute to the malignant phenotype. This is the maino acid sequence of a variant of human six transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes a composition comprising a substance that modulates the status of a protein (I) of 340 or 283 amino acids, or of any of the 15 sequences of 259 amino acids, given in the specification, or a molecule that is modulated by the protein, where the status of the cell that expresses the protein is modulated. The compositions, proteins, polynucleotides and methods are useful for treating and detecting cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 258
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STEAP-1-related
                                                                                                                                                                                                                                                                                                                                                              (AGEN-) AGENSYS INC.
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                                                                                                                                                                  53; Page 169; 248pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WKMKPRRNLEEDDYL
                                                                                                                                                                                                                                                                                                                   Ge ₩,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 comprising a substance that modulates the status of protein, useful for treating and detecting cancer.
                                                                                                                                                                                                                                                                                                                     Raitano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the
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                                                                                                                                                                                                                                                                                                                 Challita-Eid PM,
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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generating cancer
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                                                                                                                                                                                                                                                                                                                 Jakobovits
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  vaccines
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RESULT 12
ABU98392
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Best Local
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                      The invention describes a composition comprising a substance that modulates the status of a protein [1] of 340 or 283 amino acids, or of any of the 15 sequences of 259 amino acids, given in the specification, or a molecule that is modulated by the protein, where the status of the cell that expresses the protein is modulated. The compositions, proteins, polynucleotides and methods are useful for treating and detecting cancer. The STRAP-1-related proteins are useful for generating cancer vaccines. The polynucleotides are useful as tools for delineating, with greater precision, cytogenetic abnormalities in the chromosomal region that encodes STRAP-1 that may contribute to the malignant phenotype. This is the amino acid sequence of a variant of human six transmembrane epithelial antigen of the prostate or STRAP-1
                                                                                                                                                                                                                                                     New composition comprising a substance that modulates the status STEAP-1-related protein, useful for treating and detecting cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human gene
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                                                                                                                                                                                                                                                                                                                                                                              (AGEN-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                  2003-313240/30.
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                                                                                                                                                                                                                                                                                                                                                                              AGENSYS
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                                                                                                                                                                                                                                                                                                                                             Ge W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                Raitano
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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1.7e-06;
                                                                                                                                                                                                                                                                                                                                               Jakobovits
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                                                                                                                                                                                                                                                                      of a
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Query Match
Best Local Similarity
Matches 15; Conserv

Conservative

0

Mismatches

100.0%;

Score 86; DB 6; Pred. No. 1.7e-06;

Length 258;

Indels

0

Gaps

0;

Sequence

258

ΑA;

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RESULT 13
ABU98387
ID 98387
ID 98198
XX ABU98
XX ABU98
XX ABU98
XX STEAL
KW Cance
XX WO200
XX WO200
XX WO200
XX WO200
XX Homo
XX WO200
XX WO200
XX WO200
XX IAGE
XX WPI;
DR N-PS
XX WPI;
DR N-
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RESULT 14
ABU98393
ID ABU98
XX
AC ABU98
XX
AC ABU98
XX
DT 31-JU
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New composition comprising a substance that modulates the status of STEAP-1-related protein, useful for treating and detecting cancer.
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05-APR-2002; 2002US-0370387P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human gene STEAP-1 variant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example
                                                                                                                                                                                                                                                                                                                    Sequence 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AGEN-) AGENSYS
   31-JUL-2003
                                     ABU98393;
                                                                          ABU98393 standard;
                                                                                                                                                                                                                                                                                                                                                         epithelial antigen of the prostate or STEAP-1
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                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                      AA;
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Pred. No. 1.7e-06;
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RESULT 15
ABU98390
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Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or a molecule that is modulated by the protein, where the status of the cell that expresses the protein is modulated. The compositions, proteins, polymucleotides and methods are useful for treating and detecting cancer. The STEAP-1-related proteins are useful for generating cancer vaccines. The polymucleotides are useful as tools for delineating, with greater precision, cytogenetic abnormalities in the chromosomal region that encodes STEAP-1 that may contribute to the malignant phenotype. This is the amino acid sequence of a variant of human six transmembrane epithelial antigen of the prostate or STEAP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STEAP-1; six transmembrane epithelial antigen of the prostate; cancer; cancer vaccine; delineation; cytogenetic abnormality; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human gene STEAP-1 variant 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes a composition comprising a substance that modulates the status of a protein (I) of 340 or 283 amino acids, or of any of the 15 sequences of 259 amino acids, given in the specification, or a molecule that is modulated by the protein, where the status of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-SEP-2001; 2001US-0317840P
05-APR-2002; 2002US-0370387P
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                    STEAP-1; six transmembrane epithelial antigen of the prostate; cancer; cancer vaccine; delineation; cytogenetic abnormality; cytostatic;
                                                                                                                                         31-JUL-2003
                                                                                                                                                                                                                                   ABU98390 standard;
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                                                                                       Novel human gene STEAP-1 variant 8.
                                                                                                                                                                                      ABU98390;
vaccine.
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                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                comprising a substance that modulates the status o protein, useful for treating and detecting cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein,
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                                                                                                                                                                                                                                 protein; 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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WO2003022995-A2

Homo sapiens.

20-MAR-2003

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Search completed: July 12, 2004, 14:07:22 Job time: 33.9651 secs
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                                                                                                                                    Query Match
Best Local S
Matches 15
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                                                                                                                                                                                                      Sequence 258 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New composition comprising a substance that modulates the status of a STEAP-1-related protein, useful for treating and detecting cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-313240/30.
N-PSDB; ACD02604.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Fig 2H; 248pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AGEN-) AGENSYS INC.
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05-APR-2002; 2002US-0370387P.
                                                                                                                                     15;
                                                                    14
                                                                                      1 WKMKPRRNLEEDDYL 15
                                                                                                                                                     Similarity
                                                               WKMKPRRNLEEDDYL 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ge W, Raitano
                                                                                                                                  100.0%; Score 86; nilarity 100.0%; Pred. No. Conservative 0; Mismatch
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                                                                                                                                    Mismatches
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Scoring table:
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seq length: 2000000000
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_inverteb
5: sp_inverteb
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel1
9: sp_phage:*
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116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	80	7	9	υı	4	ω	Ŋ	1	Result No.
48	48	48	48	48	48	48	49	50	68	68	68	94	94	94	108	Score
41.4	41.4	41.4	41.4	41.4	41.4	41.4	42.2	43.1	58.6	58.6	58.6	81.0	81.0	81.0	93.1	Query Match
488	488	487	487	456	388	172	764	172	490	490	489	339	339	339	338	Query Match Length
4	4	4	4.	4	16	16	16	16	4	4	11	11	11	11	9	DB
Q86SF6	Q9NVB5	Q8NEW6	Q8TF03	Q8TDP3		Q938L7			Q8IUE7	Q8NFT2	Q8BWB6	Q9CWR7	Q924Z2	Q924J9	Q9GL50	ID
Q86sf6 homo sapien	Q9nvb5 homo sapien	Q8new6 homo sapien	Q8tf03 homo sapien	Q8tdp3 homo sapien	Q9a0p6 streptococc	Q93817 streptococc	Q7ul83 rhodopirell	Q8nzr1 streptococc	Q8iue7 homo sapien	Q8nft2 homo sapien	Q8bwb6 mus musculu	Q9cwr7 mus musculu	mus	Q924j9 mus musculu	Q9g150 sus scrofa	Description

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5	46.5	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	48	4.8	48
40.1	40.1	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	41.4	41.4	41.4
657	437	1652	947	912	806	763	763	763	749	889	675	568	565	442	442	442	439	438	434	431	431	429	427	233	172	929	676	498
16	N	4	12	12	10	10	10	10	4	10	w	4	w	16	16	16	16	16	16	17	16	16	16	10	16	12	13	4.
Q8NZ96	Q93TY7	Q9C0F0	Q9QAP7	104080	Q9LWM2	Q9FU78	Q9LGD6	Q9LWI2	Q8NB24	Q7XUG5	Q9UUE5	Q96MU3	Q04600	Q7TUC3	Q7TUY7	Q7VCE0	Q7UG05	Q7TTV8	Q8F4H9	Q9HMR3	Q89V23	Q8KES8	Q8R872	Q7XJP5	Q8ES61	Q9QAP4	Q7ZV52	Q7Z389
Q8nz96 streptococc	Q93ty7 shigella fi	Q9c0t0 homo sapien		Q8qv01 buffalo her		Q9fu78 oryza sativ	Q9lgd6 oryza sativ	oryza	Q8nb24 homo sapien	Q7xug5 oryza sativ	Q9uue5 schizosacch			ω		_	Q7ug05 rhodopirell	-	Q8f4h9 leptospira		Q89v23 bradyrhizob	Q8kes8 chlorobium		Q7xjp5 arabidopsis			Q7zv52 brachydanio	

ALIGNMENTS

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RESULT 1
Q9GLD
1D Q9GL
AC Q9GL
DT 01-M
DT 01-M
DT 01-J
DE Six
OS Sus
OC Buka
OC Mamm
OC Mamm
OC MCBI
RN [1]
RN [1]
RN [1]
RN EQU
RA Hesil
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RESULT 2
Q924J9
ID Q924
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Best Local 8
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Q924J9;
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Nagasaka T., Boulday G., Coupel S., Coulon F., Tesson L.,

Nagasaka T., Boulday G., Coupel S., Coulon F., Tesson L.,

Heslan J.-M., Soullillou J.-P., Charreau B.;

"Differential gene expression in endothelial cells during TNF-alpha-
and LPS-mediated activation.";

Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF319659; AA633868.1; -.

EMBL; AF319659; AA633868.1; -.

EMGG. GO.:0016021; C:integral to membrane; IEA.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Six transmembrane endothelial antigen of PAEC.
Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9GL50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane.
SEQUENCE 338 AA;
                                                                                                             Q924J9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
20; Conserv
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   (TrEMBLrel. 19, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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90.9%;
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   Last sequence update)
                                           Created)
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Q924Z2;
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                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (APR-2001) to the EMBL; AY029584; AAK50537.1; MGD: MGI:1917608; Steap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of human STEAP.";
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Mammalia; Eutheria;
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MEDLINE=21371909; PubMed=11479226;
Yang D., Holt G.E., Velders M.P., Kwon E.D., Kast W Yang D., Holt G.E., Velders M.P., Kwon E.D., Kast W "Murine six-transmembrane epithelial antigen of the stem cell antigen, and prostate-specific membrane a specific cell-surface antigens highly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Serru V., Manivet
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EMBL; AF297098; AAK83126.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Prostate and non-prostate expression of dudulin, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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Six-transmembrane epithelial
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Shkai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., Ge Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchiomni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Scheenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Manyashaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Query Match
Best Local Similarity
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01-MAR-2003 (TrE
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Weakly similar t
                                                                                         InterPro; IFKUV.
Pfam; PF03807;
                                                                                                                                                                                                  EMBL;
                                                                              SEQUENCE
                                                                                                                                                EMBL; AK052981; BAC35230.1; -. MGD; MGI:1921301; 4921538B17Rik. GO; GO:0006118; P:electron transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                          the RIKEN Genome Exploration Research Group Phase I & II "Analysis of the mouse transcriptome based on functional 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                   MEDLINE=22354683; PubMed=12466851; The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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Hayashizaki Y.;
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AA; 55760 MW;
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 Mismatches

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Pred. No.
Score 68;
Pred. No.
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98CD63D59DDDF24C
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01-OCT-2002
01-OCT-2002
01-JUN-2003
                             Cancer.";
J. Biol. Chem. 277:36689-36696(2002).
EMBL; AY008445; AAG32149.1; -.
GO; GO:0006118; P:electron transport;
InterPro; IPR004455; NADPoxred_F420.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Porkka K.P., Helenius M.A., Visakorpi T.;
"Cloning and characterization of a novel six-transmembrane protein
STEAP2, down-regulated in androgen-independent prostate cancer.";
Submitted (DEC-2001) to the EMBI/GenBank/DDBJ databases.

EMBI; AF455138; AAN04080.1; -.
Genew; HGNC:17885; STEAP2.
Go; GO:0016021; C:integral to membrane; IEA.
GO; GO:001618; P:electron transport; IEA.
InterPro; IPR004455; NADPoxred_F420.
Pfam; PF03807; F420_oxidored; I.
                                                                                                                            MEDLINE=22229309; PubMed=12095985; Korkmaz K.S., Elbi C.C., Korkmaz C Saatcioglu F.; "Molecular cloning and characteriz
                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003
01-MAR-2003
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Mammalia; Eutheria;
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(TrEMBLrel. 24, Last annotation update)
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AA; 56027 MW;
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STRAIN-MGAS8332 / Serotype M18;

MEDIINE-21927593 / PubMed=11917108;

Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., Kapur V., Daly J.A., Veasy L.G., Musser J.M.;

"Genome sequence and comparative microarray analysis of serotype
                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
101-OCT-2003 (TrEMBLrel. 25, Created)
101-OCT-2003 (TrEMBLrel. 25, Last sequence update)
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InterPro; IPR003115; ParBc.
Pfam; PF02195; ParBc; 1.
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    MEDLINE=22735913; PubMed=12835416,
                                                                                    SEQUENCE FROM
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GO:0008152; P:metabolism; IEA.
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L; AE010086; AAL98305.1; -.

GO:0005727; C:extrachromosomal

GO:0003824; F:catalytic activit
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Q938L7;
01-DEC-2001
01-DEC-2001
01-OCT-2003
                                                                                                                                         of S. pyogenes SSI-1, SF370 and MGASB232.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY050245; AAL15065.1; -.
EMBL; AB041460; AAM79843.1; -.
EMBL; AP005143; BAC63720.1; -.
EMBL; AP005143; BAC63720.1; -.
GO; GO:0005727; C:extrachromosomal circular DNA; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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                                                                                                                                                                                                                                                                                Hayashi H., Hamada S.;
Hayashi H., Hamada S.;
"The genome of invasive Streptococcus pyogenes; a comparative analysis
of a muonenes SSI-1, SF370 and MGAS8232.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schlievert P.M., Musser J.M.; "Genome sequence of a serotype M3 strain of group A phage-encoded toxins, the high-virulence phenotype,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES=S.pyogenes; STRAIN=MGAS315 / Serotype M3;
MEDLINE=22133808; PubMed=12122206;
Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
                                                                                                                                                                                                                                                                                                                                                                         SPECIES=S.pyogenes; STRAIN=SSI-1 / Serotype M3; Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Y Yamazaki K., Okahashi N., Kawabata S., Yasunaga T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES-S.pyogenes; STRAIN=NIH1; Ikebe T., Wada A., Inagaki Y., Sugama K., Tanaka D., Suz Katsukawa C., Fujinaga Y., Abe Y., Watanabe H.; "Complete sequence of temperate phage PhiNIH1.1."; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                  Pfam, PF02195; ParBc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  emergence.";
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Schlesner H., Amann R., Reinhardt R.;
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BX294150; CAD76394.1; -.
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                                                 l protein; Complete
172 AA; 19484 MW;
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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A., Borzym K., Heitmann K., Rabus R.,
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Γ., Hattori
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002295; D21N6_mtfrase.
InterPro; IPR001091; Met_trans_CN4.
InterPro; IPR002941; N6/N4_Mtase.
InterPro; IPR002925; N6_Mtase.
InterPro; IPR0021052; N6_Mtase.
InterPro; IPR003115; ParBo.
Pfam; PF01555; N6_N4_Mtase; 1.
Pfam; PF01595; ParBo; 1.
                                                                                                                                                                              Q8TDP3;
Q8TDP3;
01-JUN-2002
01-JUN-2002
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01-JUN-2001
01-JUN-2001
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21192684; PubMed=11296296; Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.M., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.; "Complete genome sequence of an M1 strain of Streptococcus pyogenes."; proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
  SEQUENCE FROM N.A.
                                     NCBI_TaxID=9606;
                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                            Homo sapiens (Human)
                                                                                                                                    PHYDE II.
                                                                                                                                                           01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00092; N6 MTASE; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 388 AA; 43690 MW; 12587B620606EBE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00506; D21N6MTFRASE.
PRINTS; PR00508; S21N4MTFRASE.
SMART; SM00470; ParB; 1.
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GO; GO:0005727; C:extrachromosomal circular DNA;
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0008170; F:N-methyllransferase activity; 1
GO; GO:0006306; P:DNA methylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

CHEST N.S. ATCC 700294 / Serotype M1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical phage associated protein. SPY0679.
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                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                  Chordata;
Primates;
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38.1%;
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Pred. No.
                                                                  Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                  43
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13;
                                                                                       Vertebrata; Euteleostomi;
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                                                                    Hominidae;
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RESULT 13
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Matches
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01-OCT-2002
01-JUN-2003
    SEQUENCE FROM N.A.

ILU Y., Beheshti B., Squire J.A., Yang X.J.,

"Characterization of a novel apoptosis-inducing gene, hg
inhibits prostate cancer cell growth.";

Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PFO
PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Steiner M.S., Allay J.A., Wang C.;
"A novel prostate-derived tumor suppressor.";
submitted (FBB-2000) to the EMBL/GenBank/DDBJ
EMBL; AP238864; AAL78206.1;
-GG; GO:0006118; Pelectron transport; IEA.
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                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                 PHyde.
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01-JUN-2002
01-JUN-2003
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InterPro; IPR004455; NADPoxred_F420
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  AY082673;
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TE; PS00290; IG MHC; 1.
NCE 456 AA; 50430 MW; C
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8; Conserv
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                                                                                                                                                            Catarrhini;
                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
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EMBL; AY029585; AAK50538.1; -.
GO; GO:0006118; P:electron transport;
                                                                                                                                                                                                 Hypothetical protein. SEQUENCE 488 AA; 5
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InterPro; IPR004455; NADPoxxed F420.
Pfam; PF03807; F420 oxidored; T.
PROSITE; PS00290; IG MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                            Vaubourdolle M., Kellermann O., Loric S.,
"Dudulin 2, a new tumor antigen expressed in Submitted (APR-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isogal T., Ota T., Hayashi K., Sugiyama T., Otsuki T. Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshik Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto Nakamura Y., Nagahari K., Masuho Y., Sasaki N.; "NEDO human cDNA sequencing project."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISOGAI T., Ota T., Hayashi K.,
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein FLJ10829 (Dudulin 2).
Homo sapiens (Human).
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InterPro; IPR004455; NADPoxred F420.
Pfam; PP03807; F420 oxidored; T.
PROSITE; PS00290; IG MHC; 1.
SEQUENCE 487 AA; 54501 MW; E0EF9
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165.853 Million cell updates/sec
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116
1 REVIHPLATSHQQYFYKIPILV 22
SwissProt_42:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Z C	Score	Query Match	Length	DB	ID	Description
1	116	100.0	339	ᆸ	STEA HUMAN	Q9uhe8 homo sapien
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7	46	•	1839	μ	CYAA_SACKL	6 saccharomy
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9	45		2549	ш	FRAP_MOUSE	mus muscul
10	44.5		137	۳	SPMI_PIG	sus
11	4.	38.4	308	μ	PYRB_METAC	5
12	44.5	•	1176	۲	RPB2_DROME	P08266 drosophila
13	44		811	μ.	RFX1 YEAST	
14	44	•	928	ᆫ	VGLB_HSVBP	
15	44		932	۲	VGLB_HSVBC	P12640 bovine herp
16	43.5		326	μ	YJHS_ECOLI	escheri
17	43	•	337	۲	DHAS_VIBCH	P23247 vibrio chol
18	43		373	_	EXT1_ARATH	arabidopsi
19	43		385	۲	GBA5_CAEEL	
20	42.5	•	299	<u> </u>	PYRB_ARCFU	
21	42		216	۲	MSRA XYLFA	
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equence update) nnotation update) nnotation update) antigen of prostate. Craniata; Vertebrata; E ; Catarrhini; Hominidae; EB873B; n E., Rastegar S., Leong Afar D.E.H.; Kuo J., Raitan Afar D.E.H.; Call-surface antigen high . 96:14523-14528(1999). Langston Y., Maupin R. EMBL/GenBank/DDBJ databas M., Grouse L.H., Derge J. Wagner L., Shenmen C.M., Wagner L., Shenmen C.M., wetow K.H., Schaefer C.F. re T., Max S.I., Wang J., Farmer A.A., Rubin G.M., odergren E.J., Malek J.A., onaldo M.F., Casavant T., ronaldo M.F., Schaefer C.F., re T., Max S.I., Mary M.F., re T., Max S.I., Mary M.F., re T., Max S.I., Mary M.F., re T., Mary M.F	W YEAST CAEEL CAEEL BUTFI B MUTFI B MUTFI D SALDU D SALDU M YEAST C PROMP C PROMP O YEAST LISMO ALIGNMENTS
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non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/

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01-NOV-1995 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
CitXC protein [Includes: Apo-citrate lyase phosphoribosyl-dephospho-
COA transferase (EC 2.7.7.61) (Holo-citrate lyase synthase) (Apo-ACP
nucleodityltransferase); 2-(5''-triphosphoribosyl)-3'-
nucleodityltransferase); 2-(5''-triphosphoribosyl)
                                                                                                                                                                                                                                                                                                                                               Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weldman J.F., Phillips C.A., Sprigs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyangs T., Hedblom E., Cotton M.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Genem C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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GO; GO:000591; C:intercellular junction; TAS.
GO; GO:0015267; F:channel/pore class transporter activity; TAS.
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EMBL; AC005053; AAC79150.1;
EMBL; AC004969; AAD15620.2;
EMBL; BC011802; AAH11802.1;
Genew; HGNC:11378; STEAP.
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STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
Fleighmann D Adams M D Whi
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Pasteurellaceae; Haemophilus.
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'(gamma charm') and a learn's protein (By similarity).

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POTENTIAL.
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                                                                                                                                                                                                                                                                                             assembly of
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                                                                                                                                                                                                                                                                                               Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
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                                                                                                                                                                                                                 formation of
                                                                                                                                      holo-acyl
                                                                                                                                                               carrier
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RESULT
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                                                                                                                                                         28-FEB-2003
28-FEB-2003
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Peptide methionine sulfoxide reductase msrA (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9HQG0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MSRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HALNI
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HAMAP; MF_00398; fused; 1.

InterPro; TPR002736; CitG.

InterPro; TPR0052751; CitX.

Pfam; PF01874; CitG; 1.

Pfam; PF03802; CitX; 1.

Transferase; Nucleotidyltransferase; Multifunctional enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      + +
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                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Halobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      methionine-S-oxide reductase)
MSRA OR VNG1180G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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TIGR; HI0021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archaea; Euryarchaeota; Halobacteria;
Halobacteriaceae; Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                      FUNCTION: Has an important function as a repair enzyme for proteins that have been inactivated by oxidation. Catalyzes the reversible oxidation-reduction of methionine sulfoxide in protein methionine (By similarity).

CATALYTIC ACTIVITY: Protein L-methionine + oxidized thioredoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    triphosphoribosyl)-3'-dephospho-CoA + adenine SIMILARITY: In the N-terminal section; belongs SIMILARITY: In the C-terminal section; belongs
               protein L-methionine S-oxide + reduce SIMILARITY: Belongs to the msrA Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEPHOSPHO-COA TRANSFERASE.
2-(5''-TRIPHOSPHORIBOSYL)-3'-
DEPHOSPHOCOENZYME-A SYNTHASE.
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               sulfoxide reduc
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RESULT 4
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Best Local S
Matches
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01-OCT-1996
01-OCT-1996
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between
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Oxidoreductase; Complete proteome.
ACT_SITE 12 BY SI
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Pfam; PF01625; PMSR; 1.
ProDom; PD003489; PMSR; 1.
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                                                                                                                                                                                                                                                                                                                       Plant
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                                                                                                                                                                                                                                                                                                                                                               STRAIN=Avonport;
Reith M.E., Munholland
                                                                                                                                                                                                                                                                                                                                                                                                               sukaryota; Rhodophyta;
NCBI_TaxID=2787;
                                                                                                                                                              between
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                                                                                                                                                                                                                                                                                                                                     genome.
                                                                                                                                                                                                                                                                                                                                                   "Complete nucleotide
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apocytochrome f precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003
                                                                                           or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Porphyra purpurea
             HAMAP; MF_00610; -; :
InterPro; IPR002325;
                                                    PIR; S73186; S73186.
                                                                                                                                    European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                FUNCTION: Translocates protons across the thylakoid membrane and transfers electrons from photosystem II to photosystem I. It receives electrons from the Rieske iron-sulfur protein and passes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PORPU
                                                                                                                                                                                                     SIMILARITY: Belongs to the cytochrome c family.
                                                                                                                                                                                                                             protein (By similarity).
SUBCELLULAR LOCATION: Chloroplast thylakoid membrane.
                                                                                                                                                                                                                                                         SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                  them to plastocyanin.
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                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a cen the Swiss Institute of Bioinformatics and the EMBL
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                                         P36438;
                                                                 U38804; AAC08151.1;
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and this statement
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                                                                                             email
                                                                                                                                                                                                                                                                                                                         Biol. Rep. 13:333-335(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                (By similarity)
                                                                                                                                                                                                                                                      Interacts with plastocyanin and Rieske iron-sulfur
                                         1HCZ.
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                                                                                           license@isb-sib.ch).
Apocyt_F.
CytC_heme_BS
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                                                                                                                                                                                                                                                                                                                                                   sequence of the Porphyra purpurea chloroplast
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ID SYFA, A
AC 09T034
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RA Weichselgartner M., de Simone V., Dbermaler B., Mache R., Mueller M., RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T., RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I., RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I., J. Zimmermann W., Wedler H., Ridley P., RA Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P., RA Langham S.-A., McCullagh B., Bilham L., Robben J., Vandenbussche F., RA Langham S.-A., McCullagh B., Bilham L., Robben J., Vandenbussche F., RA Langham S.-A., McCullagh B., Bilham L., Robben J., Vandenbussche F., RA Meitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M., RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W., RA Mocijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P., RA Montagu M., Rogers J., Cronin A., Quall M.A., Bray-Allen S., RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R., RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R., RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S., RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S., RA Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E., RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R., RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R., RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A., RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A., RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S., Rahelke C., Faccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
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Best Local
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METAL
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PRINTS; PR00610: CYMOCHBONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9TO34; Q8LPR1;
16-OCT-2001 (Rel. 40, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Probable phenylalanyl-tRNA synthetase alpha chain
(Phenylalanine-tRNA ligase alpha chain) (Phers).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae: Arabia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Photosystem I;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volcka. Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terr Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M. Weichselgartner M., de Simone V., Obermaier B., Mache R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20083488; PubMed=10617198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=cv.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REIIFPILSPDPAKDKQAHFFKYPIYV
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Pred. No. 3
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NITROGEN) (BY SIMILARITY)
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A Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
A Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
A Karlin-Newmann G., Liu S.K., Lam B., Sakano H., Wu T., Yu G.,
A Karlin-Newmann G., Liu S.K., Lam B., Sakano H., Wu T., Yu G.,
A Karlin-Newmann G., Liu S.K., Lam B., Sakano H., Wu T., Yu G.,
A Karlanda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
A Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
A Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
A Arakawa T., Banh J., Banno F., Bowser I., Brooks S.Y., Carninci P.,
A Arakawa T., Banh J., Banno F., Bowser I., Hrooks S.Y., Carninci P.,
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A Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
A Khan S., Koesema E., Tshida J., Jiang P.X., Jones T., Kawai J.,
A Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
A Satrou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,
"Empirical analysis of transcriptional activity in the Arabidopsis
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                                                                                                                           Matches
                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P27001; 12...
InterPro; IPR004529; PheS.
InterPro; IPR002319; tRNA-synt_2d.
InterPro; IPR006195; tRNA ligase II.
                                                                                                                                                                                                                                                      Pfam; Pro1409; trNA-synt 2d; 1. TIGREPAMS; TIGRO0468; pheS; 1. TSTARO0468; pheS; 1. 1. PROSITE; PS50862; AA_TRNA_LIGASE II; 1. Aminoacyl-trNA synthetase; Protein biosynthesis; Ligase; SEQUENCE 485 AA; 55792 MW; 9EAOCO360CA3F9DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL050351; CAB43643.1; ALT_SEQ.
EMBL; AL161994; CAB80591.1; ALT_SEQ.
EMBL; AV094460; AAM19830.1; -.
EMBL; BT002310; AAN73307.1; -.
HSSP; P27001; 1PYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genome.";
Science 302:842-846(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = diphosphate + L-phenylalanyl-tRNA(Phe).
-i- SUBUNIT: Tetramer of two alpha and two beta chains (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22954850; PubMed=14593172;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to class-II aminoacy1-tRNA synthetase family.
Phe-tRNA synthetase alpha chain subfamily 2.
CAUTION: Ref.1 sequences differ from that shown due to erroneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene model prediction.
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                                                                                                                                                           Similarity
HPLATSHQQYFYKIP 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           equires a license agreement (S email to license@isb-sib.ch).
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                                                                                                                       Conservative
                                                                                                                                                   39.7%;
46.7%;
                                                                                                           Score 46; DB
Pred. No. 9.9;
2; Mismatches
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                                                                                                               6
                                                                                                                                                                                  Length 485;
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RESULT 6
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ID GLGE M
AC 010638
DT 01-0CT
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OS MYCODA
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                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the Buropean Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fic entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Garnier T., Biglmeier K., Camus J.-C., Medina N., Mansoor H.,
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
-i- FUNCTION: Could be involved in glycogen catabolism (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLGE MYCTU
Q10638;
01-OCT-1996
28-FEB-2003
10-OCT-2003
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Davies R., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";

Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES=M.bovis; STRAIN=AF2122/97; MEDLINE=22709107; PubMed=12788972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=2206494; PubMed=12218036; Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.; "Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterineae; Mycobacteriaceae; Mycobacterium NCBI_TaxID=1773, 1765;
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GLGE OR RV1327C OR MT1369 OR MTCY130.12C OR MB1362C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Belongs to family 13 of glycosyl hydrolases. GlgE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         subfamily.
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(Rel. 42, Last annotation update)
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TIGR; MT1369; -.
TubercuList; Rv1327c;

IPR006589; Alp_amyl_cat_sub

Z73902; CAA98091.1; ALT INIT AE007010; AAK45633.1; ALT IN BX248338; CAD94223.1; -.

http://www.isb-sib.ch/announce/

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P23466;
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MEDLINE=9133718; PubMed=1864503;
Young D., O'Neill K., Broek D., Wigler M.;
Young D., O'Neill K., Broek D., Wigler M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi;
Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1991
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                                                                                                                                   SMART; SM00044; CYCc; 1.
SMART; SM00369; LRR_TYP; 2.
SMART; SM00332; PP2Cc; 1.
SMART; SM00314; RA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                           PIR; JQ1145; OYBYK.
                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X56042; CAA39513.1; -.
                         Magnesium
DOMAIN
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European Bioinformatics Institute. There a
by non-profit institutions as long as i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: ATP = 3',5'-cyclic AMP + diphosphate. COPACTOR: Binds 1 magnesium ion per subunit (By similarity). SIMILARITY: Belongs to the adenylyl cyclase class-3 family. SIMILARITY: Contains 21 leucine-rich (LRR) repeats. SIMILARITY: Contains 1 PP2C-like domain. SIMILARITY: Contains 1 Ras-associating domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e adenylyl cyclase-encoding gene from Saccharomyce
e 102:129-132(1991).
FUNCTION: Plays essential roles in regulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 metabolism by catalyzing the synthesis
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0128; alpha-amylase; 1.
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Leucine-rich
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42, Last annotation update)
(EC 4.6.1.1) (ATP pyrophosphate-lyase) (Adenylyl
                                                                                                         GUANYLATE_CYCLASES_2;
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WEDLINE=20083488; PubMed=10617198;

WADLINE=20083488; PubMed=10617198;

Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,

Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M.,

WHARTIS B., Ansorge W., Brandt P., Grivell L.A., Rieger M.,

Walchest B., Potetes B., Prezz-Alonso M., Boutry M., Bancroft I.,

Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,

Kreis M., Delseny M., Puigdomenech P., Watson M., Boutry M., Bancroft I.,

Walchert B., Pottetelle D., Perez-Alonso M., Boutry M., Bancroft I.,

Walchert B., McCullagh B., Bilham L., Robben J.,

Wan der Schweren J., Czymmuprez B., Chuang Y.-J., Vandenbussche F.,

Walcher Schweren J., Grymmuprez B., Chuang Y.-J., Vandenbussche F.,

Walcher E., Brandt A., Peters S., van Staveren M., Ditkse W.,

Walcher E., Brandt A., Peters S., van Staveren M., Ditkse W.,

Walcher E., Brandt A., Feldpausch M., Lamberth S., Van den Daele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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SEQUENCE
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SEQUENCE FROM N.A.
STRAIN=cv. Columbia; TISSUB=Flower;
Ulker B., Kushnir S., Somssich I.E.;
"Arabidopsis thaliana transcription factor WRKY13.";
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                                                                                                                                                                                                                                                               Bukaryota; viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                               10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable WRKY transcription factor 13 (WRKY D.
WRKY13 OR AT4G39410 OR F23K16.40.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                       WR13
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                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
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8; Conserv
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Pred. No. 42;
1; Mismatches
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MAGNESIUM
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CATALYTIC.
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NESIUM (BY SIMILARITY)
86A69BCB1F2733CB CRC6
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RA Chefdor F. Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francs P., Bielke C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bedhia N., Ghoj L., Schutz K., Huang E., Spiegel L.,
RA Zaccaria P., Bedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Schon M., Murray J., Sheet P., Cordes M., Abberthacieh J.,
RA Schon M., Murray J., Sheet P., Cordes M., Abberthacieh J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Swaby I.X., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
Far Chen B., Marra M.A., Martienssen R., McCombie W.R.,
Farliana "... Shondy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
Far Chen B., Marra M.A., Martienssen R., McCombie W.R.,
                                                                                                                                                                                                                                                                Matches
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Best Local
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FRAP MOUSE STANDARD;
Q9JLN9;
16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AP421153; AAL13042.1; -.
EMBL; AL078620; CAB44676.1; -.
EMBL; AL161595; CAB80604.1; -.
PIR; T09357; T09357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF03106; WRKY; 1. PROSITE; PS50811; WRKY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 402:769-777(1999).

-!- FUNCTION: Transcription factor. Interacts specifically with the box (5'-(T)TGAC(C(T)-3'), a frequently occurring elicitor-responsive cis-acting element (By similarity).

-!- SUBCELLULAR LOCATION: Nuclear (Probable).

-!- SIMILARITY: Belongs to the WRKY group II-c family.

-!- SIMILARITY: Contains 1 WRKY domain.
                                                                                                                                                                                                                                                                                                                                                                                               Transcription regulation; DNA-binding; DOMAIN 31 98 SER-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a continuous the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interPro; IPR003657; WRKY.
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                                                                                                                                                                                                                                                              Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                    304 AA;
                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                  34203 MW;
                                                                                                                                                                                                                                                                                 38.8%;
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                                                                                                                                                                                                                                                                               Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                          WRKY
                                                                                                                                                                                                                                                                                                                                                  589ECCAC35F28017 CRC64;
                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                   Nuclear protein
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S.,
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Best Local
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GG:0007281; P:germ-cell developmen
GG:0007281; P:germ-cell developmen
InterPro; IPR008938; ARM.
InterPro; IPR003151; FAT.
InterPro; IPR003151; FATC.
InterPro; IPR003157; HEATC.
InterPro; IPR000357; HEATC.
InterPro; IPR000309; PI3 PI4 kinase.
InterPro; IPR008940; Premyl_Trans.
Pfam; PF02250; FATC; 1.
Pfam; PF02250; FATC; 1.
Pfam; PF02260; FATC; 1.
SMART; SM00146; PI3 PI4 kinase; 1.
SMART; SM00146; PI3 PI4 kinase; 1.
                            SPMI_PIG
Q28920;
16-OCT-2001
                                                                                                   PIG
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DOMAIN
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
REPEAT
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"Positional cloning of mouse plasmacytoma susceptibility gene.";

Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

-!- FUNCTION: ACTS AS THE TARGET FOR THE CELL-CYCLE ARREST AND

IMMUNOSUPPRESSIVE EFFECTS OF THE FKBP12-RAPAMYCIN COMPLEX.

-!- SIMILARITY: Belongs to the PIJ/PI4-kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transferase; Kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Contains 8 HEAT repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=BALB/c;
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15-MAR-2004 (Rel. 43, Last annotation updat
FKBP-rapagin associated protein (FRAP).
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(Rel. 40, Created)
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16-OCT-2001

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SIGNAL 1 21 BY (
CHAIN 22 137 SEM:
DOMAIN 30 131 CUB:
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CARBOHYD 36 36 N-LI
SEQUENCE 137 AA; 15194 MW; 9D
                                                                                                                                                                                                                                                              PYRB METAC
Q8THL2;
28-FEB-2003
                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboratio between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                         Aspartate carbamoyltransferase transcarbamylase) (ATCase). PYRB OR MA4502.
                                                                                                                                                                                                                                                                                                                                       METAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00985; SPERMADHESIN 1; PROSITE; PS00986; SPERMADHESIN 2; PROSITE; PS01180; CUB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Iwamoto T., Hiroaki H., Furuichi Y., Wada K.,
Osada T., Gagnon C.;
"Cloning of boar SPMI gene which is expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - -
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vesicle and codes for a sperm motility inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16~OCT-2001 (Rel. 40,
Seminal plasma sperm
                           NCBI_TaxID=2214;
[1]
                                                                        Methanosarcinaceae;
                                                                                         Archaea; Euryarchaeota;
                                                                                                                  Methanosarcina acetivorans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00042; CUB;
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InterPro; IPR000124; Spermadhesin.
Pfam; PF00431; CUB; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Seminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa
  SEQUENCE FROM N.A
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FUNCTION: Inhibitor of sperm motility.
SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Contains 1 CUB domain. SIMILARITY: Belongs to the spermadhesin family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; $80568; AAB3500
$72508; $72508.
                                                                                                                                                                                                                                                                                                                                                                                                                                   115
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HAMAP; MF 00001; -; 1.

InterPro; IPR006130; Asp/Orn_COtranf.

InterPro; IPR002082; Asp_carbmltransf.

InterPro; IPR006131; OTCace_O.

InterPro; IPR006132; OTCace_P.

Pfam; PF00185; OTCace_N; 1.

Pfam; PF02729; OTCace_N; 1.
                                                                                                                                                                                                                                                                                                                                                                 P0826; Q04155; Q95027; Q9VFM7;
01-AUG-1988 (Rel 08, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
10A-directed RNA polymerase II 140 kDa polypeptide
(RNA polymerase II subunit 2).

RPII140 OR CG3180.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R., Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W., Zimmer A., Barber R.D., Cann I., Graham D.B., Grahame D.A., Guss A.M., Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A., Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K., Springer T.A., Umayam L.A., White O., White R.H., de Macario B.C., Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I., Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E., Metcalf W.W., Birren B.;
                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00100; AOTCĀSĒ.
TIGRAMS; TIGRO0670; asp_carb tr; 1.
PROSITE; PS00097; CARBAMOVITĀNSFERĀSĒ; 1.
Pyrimidine biosynthesis; Transferase; Comp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C2A / ATCC 35395 / DSM 2834;
MEDLINE=21929760; PubMed=11932238;
                   TISSUE=Embryo;
MEDLINE=88011299; PubMed=3116266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                        Bphydroidea; Drosophilidae; Drosophila
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute.
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-!- CATALYTIC ACTIVITY: Carbamoyl
                                                                                                         SEQUENCE
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Dworniczak B.,
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Golale R.F.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Xandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Ge Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Davies M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cawley S., Davies M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cawley S., Davies M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cawley S., Davies M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cawley S., Davies M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Cherry J. Harris M., Calasser K.,
RA Liuk M., Calasser K., Liu J.H., J.H., Li Z., Liang Y., Lin X.,
Li J. Li J. Li J. Li Z., Liang Y., Lin X.,
Li J. Li J. Li J. Li Z., Liang Y., Lin X.,
Li J. Li J. Li J. Li J. Li Z., Liang Y., Lin X.,
RA Wellon D.R., Nelson K.A., Nixon K.
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Stepleton M., Carroll H., Kronmar,
George R.A., Guarin H., Kronmar,
Rubin G.M., Celniker S.E.;
Rubin G.M., Celniker S.E.;
"A Drosophila full-length cDNA resource.";
                                                                                                                                                                                                                                                                                                                                                                                                             Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sitzler S., Oldenburg I., Peterson G., Bautz E.K.F.; "Analysis of the promoter region of the housekeeping gene DmRP140 sequence comparison of Drosophila melanogaster and Drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Berkeley; TISSUE=Embryo;
MEDLINE=22426066; PubMed=12537569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91276237; PubMed=1905256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20196006; PubMed=10731132;
                                                                                                                DIFFERENT POLYPEPTIDES
                                                                                                                                                           {RNA}(N).
SUBUNIT: EACH CLASS
                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                             FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
                                           POLYMERASE
                                                                                                                                                                                                                                                                                    substrates.
                                                                                                                                                                                                                                                                                                                                                                                                                 100:155-162(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polymerase II of Drosophila. Relation of its 140,000 Mr subunit
                                                                                                                                                                                                                                                                                                                      DNA into RNA using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   beta subunit of Escherichia coli RNA polymerase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carlson J.W., Brokstein P., Yu C., Champe M., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
                                                                             THIS SUBUNIT IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195:929-937(1987).
LOCATION:
                                                                     OF RNA POLYMERASE IS ASSEMBLED FROM 9 TO 14
DES. RNA POLYMERASE II CONSISTS OF 10 DIFFERENT
NIT IS THE SECOND LARGEST COMPONENT OF RNA
                                                                                                                                                                                                                                                                                                                           the four ribonucleoside
                                                                                                                                                                                                                                                                                                                           triphosphates
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R InterPro; IPRO07644; RNA_pol Rpb2_1.

R InterPro; IPRO07644; RNA_pol Rpb2_2.

R InterPro; IPRO07645; RNA_pol Rpb2_3.

R InterPro; IPRO07646; RNA_pol Rpb2_3.

R InterPro; IPRO07647; RNA_pol Rpb2_5.

R InterPro; IPRO07647; RNA_pol Rpb2_5.

R InterPro; IPRO07641; RNA_pol Rpb2_6.

R InterPro; IPRO07641; RNA_pol Rpb2_7.

R Pfam; PP04563; RNA_pol Rpb2_7; 1.

R Pfam; PP04565; RNA_pol Rpb2_7; 1.

R Pfam; PP04565; RNA_pol Rpb2_3; 1.

R Pfam; PP04565; RNA_pol Rpb2_3; 1.

R Pfam; PP04565; RNA_pol Rpb2_5; 1.

R Pfam; PP04567; RNA_pol Rpb2_5; 1.

R Pfam; PP04567; RNA_pol Rpb2_6; 1.

R Pfam; PP04567; RNA_pol Rpb2_6; 1.

R Pfam; PP04567; RNA_pol Rpb2_6; 1.

R Pfam; PP04560; RNA_pol Rpb2_6; 1.

R Pfam; PP04560; RNA_pol Rpb2_7; 1.

R Pfam; PP04560; RNA_pol Rpb2_7; 1.

R PROSITE; PS01166; RNA_Pol BFTA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                          P48743;
01-FEB-1996
15-JUL-1998
10-OCT-2003
                                                                                                                                                                                                                                                             YEAST
                                                      Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                01-FEB-1996 (Rel. 33, Created)
15-JUL-1998 (Rel. 36, Last sequence up
10-OCT-2003 (Rel. 42, Last annotation
RFX-like DNA-binding protein RFX1.
RFX1 OR CRT1 OR YLR176C OR L9470.18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M62972; AAA28476.1; -. PIR; A27826; A27826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no resti
                                   NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO:0005665; C:DNA-directed RNA p
GO:0003899; F:DNA-directed RNA p
GO:0006366; P:transcription from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MISCELLANEOUS: Three distinct zinc-containing RNA polymerases are found in eukaryotic nuclei: polymerase I for the ribosomal RNA precursor, polymerase II for the mRNA precursor, and polymerase III for 5S and tRNA genes.

SIMILARITY: Belongs to the RNA polymerase beta chain family. CAUTION: Ref. 1 sequence differs from that shown due to a frameshift in position 43 leading to an erroneous gene model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prediction.
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AE003703; AAF55024.1; -.
BT003265; AA025022.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                    EVIHPLATSHOOVEY-KIPILV 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FBgn0003276; RpII140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1176 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               667
                                                                                                                                                                                                                                                                                                                                                                                                                                             38.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134042 MW;
                                                                                                                                                                               Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 44.5;
Pred. No. 4
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ID -> MY (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNA polymerase II, core complex; RNA polymerase activity; NAS. n from Pol II promoter; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224821B335BED7F0 CRC64;
                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 45;
                                                                                                                                                                                                                                            AA
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Best Local S
Matches
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SGD; S0004166; RFXI
GO; GO:0005737; C:cyt
GO; GO:0005634; C:nuc
GO; GO:0016566; F:spo
GO; GO:0000122; P:nec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSVBP
VGLB HSVBP
P17471;
01-AUG-1990
01-AUG-1990
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Benes V., Brueckner M., Delius H., Dubois E., Duesterhoeft A.,
Entian K.-D., Floeth M., Goffeau A., Hebling U., Heumann K.,
Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P.,
Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D.,
Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,
Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M.,
Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S.,
Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P.,
Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E.,
Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.;
"The mucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
Nature 387:87-90(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
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MEDLINE=97313267; Pub
                                                                                                                                                                                                 Misra V., Nelson R., Smith M.;
"Sequence of a bovine herpesvirus
homologous to the herpes simplex 9
Virology 166:542-549(1988).
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=89020821; PubMed=2845660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovine herpesvirus type 1
Viruses; dsDNA viruses, no
Alphaherpesvirinae; Varice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
   between the the European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003150; RFX_DNA_birding;
                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nonline; 1*22..., s0004166; REXI.
GO:0005737; C:cytoplasm; IDA.
GO:0005634; C:nucleus; IDA.
GO:0016566; F:specific transcriptional repressor activity;
GO:000122; P:negative regulation of transcription from P.
GO:0000122; P:negative 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Belongs to the RFX family.
                                                                                                                               SUBUNIT: Dimer, probably linked SIMILARITY: Belongs to the herpe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 15, Created)
(Rel. 15, Last sequence upd
(Rel. 40, Last annotation u
n I precursor (Glycoprotein
in 16) (Glycoprotein Gl30).
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   Swiss Institute
Bioinformatics
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                                Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      type 1 (strain P8-2)
ses, no RNA stage; H
Varicellovirus.
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herpesviruses glycoprotein
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J. Virol. 62:3319-3327(1988). linked by disulfide
-!- SUBUNIT: Dimer, probably linked by disulfide
-!- STMTLARITY: Belongs to the herpesviruses glyc
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01-OCT-1989 (Rel. 12, Last sent)
16-OCT-2091 (Rel. 40, Last ann)
Glycoprotein I precursor (Glyco
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                                                                                                                                                                                       between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. They use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti
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01-OCT-1989
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                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
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MEDLINE=88300884; PubMed=2841484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Whitbeck J.C., Bello L.J., Lawrence W.C., "Comparison of the bovine herpesvirus 1 g
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16-OCT-2001 (Rel. 40, Last annotation update)
Glycoprotein I precursor (Glycoprotein GWP-6) (Glyco
(Glycoprotein 16) (Glycoprotein G130) (Glycoprotein
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DR InterPro; IPR000234; Glycoprot B.
DR Pfam, PF00666; Glycoprotein B; 1.
DR Probom; DR006693; Glycoprotein B; 1.
ET Probom; DR006693; Glycoprotein; Transmembrane; Signal.

FT SIGNAL 68 932
FT CHAIN 68 932
FT CARMAIN 828 932
FT CARROHYD 105 105 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARROHYD 105 105 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARROHYD 441 441 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARROHYD 443 A83 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARROHYD 440 640 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARROHYD 706 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 932 AA; 101195 MW; 9DCEAA85C5FC3DA3 CRC64;

Query Match 37.9%; Score 44; DB 1; Length 932;
Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Query Match 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Query Match 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Query Match 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Query Match 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Query Match 6; Conservative 5; Mismatches 6; Conservative 5; Mismatches 6; Conservative 5; Mismatches 6; Conservative 6; Search completed: July 12, 2004, 14:08:02
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Copyright (c) 1993 - 2004 Compugen Ltd.
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

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4.			233	N	D84797	hypothetical prote
υı	47	0	431	N	H84392	ă
თ	47	40.5	565	N	89	hypothetical prote
7	47		675	N	T39727	rin l
œ	46		169	N	T07623	extensin homolog
9	46		296	2	AI1178	transcription reg
10	46	9.	425	N	AD1149	O-acetylhomoserine
11	46		425	N	AD1508	O-acetylhomoserine
12	46	•	428	N	T08576	phenylalanine-tRNA
13	46	39.7	430	2	C83975	O-acetylhomoserine
14	46	39.7	735	N	AD0341	ment
15	46	39.7	737	N	C70770	hypothetical prote
16		39.7	1839	Н	OYBYK	e cyc
17	45	•	304	2	T09357	ca
18	45	•	428	N	T46025	· m
19	45		607	N	AG3323	penicillin-bind
20	44.5	38.4	136	N	S72508	sperm motility inh
21		•	1176	N	A27826	-
22	44		163	N	C91092	tical
23	44	•	163	N	G85937	ical
24	44		472	N	G81293	•
25	44	37.9	771	N	S51421	
26	44	•	928	н	VGBEBG	glycoprotein gI
27	44		932		VGBEBC	
28	44		0	ᆫ		~
)		٠	969	22 12	B87336	

45	44	43	42	41	40	9	38	37	36	35	34	ω ω	32	31	30
43	43	43	43	43	43	43	43	43	43	43	43	43	43	43.5	43.5
37.1	37.1	37.1	37.1	37.1	37.1	37.1	37.1	37.1	37.1	37.1	37.1	37.1	37.1	37.5	37.5
485	442	434	430	426	385	384	379	373	338	337	336	295	284	326	326
Ŋ	N	N	N	N	N	N	N	Ŋ	2	ш	N	N	N	N	2
T37550	T44655	AH3397	D72324	A86634	T16447	B72324	C86873	В96798	B82118	S14523	F86319	F83356	871227	G86128	D91287
hypothetical coile	O-acetyinomoserine	cysteine synthase	O-acetyinomoserin	O-acetyinomoserine	hypothetical prot	oxaloacetate decar	transcription regu	extensin [imported	probable aspartate	aspartate-semialde	Hypothetical prote	hypothetical proce		cal	

ALIGNMENTS

RESULT 1

B64140
hypothetical protein HI0021 - Haemophilus influenzae (strain Rd KW20)
hypothetical protein HI0021 - Haemophilus influenzae (c; pactes: Haemophilus influenzae
C; pactes:

A;Reference number: A84160; MUID:20504483; PMID:11016950 A;Accession: G84273 A;Accession: G84273 A;Status: preliminary A;Molecule type: DNA A:Peridines: 1-177 (STO)	<pre>Jung, K.H.; Alam, M.; Freitas, T. Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000 A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; A;Title: Genome sequence of Halobacterium species NRC-1.</pre>	C;Accession: G84273 R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, ; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jab	<pre>peptide methionine sulfoxide reductase [imported] - Halobacterium sp. NRC-1 C;Species: Halobacterium sp. NRC-1 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001</pre>	RESULT 2 G84273	Qy 1 REVIHPLATSHQQYFYKIPI 20	Query Match 45.3%; Score 52.5; DB 2; Length 416; Best Local Similarity 50.0%; Pred. No. 1.5; Matches 10; Conservative 4; Mismatches 5; Indels	A,Start codon: GTG C;Superfamily: citG protein
A;Reference number: A84160; MUID:20504483; PMID:11016950 A;Recession: G84273 A;Retus: preliminary A;Status: preliminary A;Molecule type: DNA A;Residues: 1-177 <sto> A;Residues: 1-177 <sto> A;Cross-references: GB:AE004437; NID:g10580713; PIDN:AAG19555.1; GSPDB:GN00138</sto></sto>	dt, H.; Lowe, T.M.;	Shukla, H.D.; Lasky Maddocks, D.G.; Ja	sp. NRC-1 -Feb-2001			1; Gaps 1;	

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RESULT 5
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A; Residues: 1-233 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: D84797
                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 402,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Genome: chloroplast
C;Superfamily: cytochrome f
C;Keywords: chloroplast; heme; thylakoid
                                                                                                                                                                                                                                                                                                                                                 A;Map
                                                                                                                                                                                                                                                                                                                                                                            A;Gene: At2g37810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein At2g37810 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Reith, M.; Munholland, J.
R;Reith, M.; Munholland, J.
R;Reith, M.; Munholland, J.
Rep. 13, 333-335, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytochrome f - red alga (Porphyra purpurea) chloroplast C;Species: chloroplast Porphyra purpurea
C;Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 11-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant Mol. Biol. Rep. 13, 333-335, 1995
A;Title: Complete nucleotide sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: petA
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                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                     Genetics:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Koo, H.; Moffatt, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.; S., D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Company, C.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Company, C.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C.S., D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C.S., D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C.S., D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C.S., D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C.S., D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C.S., D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C.S., D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C.S., White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C.S., White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C.S., White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C.S., White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C.S., White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C.S., White, C.S., Whit
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les 9; Conserv
                                                                                                               105
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                                                                                                                                                                                                                            l Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 REVIHPL----ATSHQQYFYKIPILV 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N
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                                                                                                            VHPLCTQHHQHVSYVP 120
                                                                                                                                                               IHPLATSHQQYFYKIP 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ETFYPAAEKHONYFEKNP 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVIHPLATSHOOYFYKIP
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                                                                                                                                                                                                                   40.5%; Score 47; ilarity 43.8%; Pred. No. Conservative 3; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                 GB:AE002093; NID:g4895203; PIDN:AAD32790.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1999
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40.7%;
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50.0%;
                                                                                                                                                                                                    Pred. No. o,
3; Mismatches
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4; Mismatches
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Pred. No. 7
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Pred. No. 2.
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                                                                                                                                                                                 nucleoporin homolog - fission yeast (Schizosaccharomyces pombe) C,Species: Schizosaccharomyces pombe C,Species: Schizosaccharomyces pombe C,Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change C,Accession: T39727
C,Accession: T39727
R,Wood, V.; Rajandream, M.A.; Barrell, B.G.; Volckaert, G. submitted to the EMBL Data Library, August 1999
                                                                                                                                                                                                                                                                                                                                                                                      RESULT
A;Cross-references: EMBL:AL109846; PIDN:CAB52802.1; A;Experimental source: strain 972h-; cosmid c17G9
                                                                                                               A;Reference number: Z21874
A;Accession: T39727
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                            A; Residues: 1-675 < WOO>
                                                                                       A; Molecule type: DNA
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A;Cross-references: A
A;Map position: 4R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein YDR117c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YD9727.12c
C;Species: Saccharomyces cerevisiae
C;Date: 19-May-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
C;Accession: S52682
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Dung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A; Anthors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, A; Title: Genome sequence of Halobacterium species NRC-1.
A; Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:Z48758; NID:g747879; PID:g747891; GSPDB:GN00004; MIPS:YDR117cC;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-565 < MUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, March
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Murphy,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE004437; NID:g10581828; PIDN:AAG20508.1; GSPDB:GN00138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues:
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     439 EILHPLLTNNFTEFYQI
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8; Conserv
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8; Conserv
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Pred. No.
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M.J.; Hough, D.W.; Maddocks, D.G.; Jablo
                              GSPDB:GN00067; SPDB:SPBC17G9.04c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
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Gaps

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T.M.;

07-Dec-1999

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Gaps

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A; Cross-referent
A; Experimental
C; Genetics:
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A;Title: Isolation and characterization of three soybean extensin cDNAs. A;Reference number: Z16058; MUID:94211912; PMID:8159793
A;Accession: T07623
                                                                                                                                                                                                                                       D.; Jones, L.M.; Karst, U.
Science 294, 849-52, 2001

A;Authors: Kreft, U.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Maduen, O., C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AI1178
A;Status: preliminary
A;Status: preliminary
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C;Superfamily: hydroxyproline-rich glycoprotein
C;Keywords: glycoprotein; hydroxyproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N;Alternate names: hydroxyproline-rich glycoprotein HRGP2
C;Species: Glycine max (soybean)
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A;Gene: SPDB:SPBC17G9.04c
                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AII178
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.;
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A;Molecule type: mRNA
A;Residues: 1-169 <HON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 11-May-2000
C;Accession: T07623
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                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-296 <G
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               8
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: EMBL:L22030; NID:g347454; Experimental source: strain Wayne; seedling
                                                                       Query Match
Best Local (
                                                                                                                                                    Genetics:
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                                                       Similarity 7; Conserv
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EVIHPLATSHQQYFYKI
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                                                     39.7%; ilarity 41.2%; Conservative
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57.1%;
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                   18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
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Pred. No.
                                                       9
                                                                       Score 46; DB
Pred. No. 11;
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                                                                                           Length 296
                                                                                                                                                                                                                                                                                                                           G.; Madueno, E.; uez-Boland, J.A.;
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Voss, H.; Wehland
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Fsihi, H
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Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J. A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1149
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C;Date: 27-Nov-2001 #sequence_revision
C;Accession: AD1149
                                                                                                                                                                                                                                                                                                                                                                                                          D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J. A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1508
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C;Superfamily:
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A;Molecule type: DNA
A;Residues: 1-425 <GLA>
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                                                                                                                                                                                                                                                            A; Gene: lin060 C; Superfamily:
                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AL592022; PIDN:CAC95836.1; PID:g16413044; GSPDB:GN00178
A;Experimental source: strain Clip11262
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A; Residues: 1-425 < GLA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Listeria
C;Date: 27-Nov-2001
C;Accession: AD1508
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phenylalanine-tRNA ligase (EC 6.1.1.20) beta chain
C;Species: Arabidopsis thaliana (mouse-ear cress)
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                                                      RESULT
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Best Local
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376 IIHPASTTHQQ 386
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                                                                                                            376 IIHPASTTHQQ 386
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                                                                                                                                               3 VIHPLATSHOO 13
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hurand, L.; Dussı
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                     T22F8.180 [similarity] -
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surget, O.;
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tian, K.D.;
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Voss, H.; Wehland
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Voss, H.; W
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Fsihi, H
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A;Gene: YP02801

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R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                           probable membrane protein YPO2801 [imported] - Yersinia pestis (strain CO92) (;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AD0341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: BH2603
C; Superfamily: O-succinylhomoserine (thiol)-lyase
A;Cross-references: GB:AL590842; PIDN:CAC93035.1; PID:g15980773; GSPDB:GN00175
                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-735 <KUR>
                                                                                                           A; Reference number: AB0001; A; Accession: AD0341
                                                                                                                              A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-430 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
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C;Superfamily: yeast cytosolic phenylalanine-tRNA ligase beta chain
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
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C;Accession: T08576
R;Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mew submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16442
A;Accession: T08576
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A;Experimental source: cultivar Columbia; BAC clone T22F8
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A; Residues: 1-428 <BEV>
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Best Local :
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ces 7; Conserv
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IIHPASTTHQQ 389
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Pred. No. 17;
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Search completed: July 12, 2004, 14:11:18 Job time: 12 secs

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A;Residues: 1-737 <COL>
A;COL>
A;Cross-references: GB:Z73902; GB:AL123456; NID:g3261576; PIDN:CAA98091.1; PID:e245021;
A;Experimental source: strain H37Rv
C;Genetics:
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                                                                                                                                                      A;Gene: Rv1327c
                                                                                                                                                                                                                                                          A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                   A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: C70770
                                                                                                                                                                                                                                                                                                                                                       R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999 C;Accession: C70770
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C;Species: Mycobacterium tuberculosis
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389
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                                   5 HPLATSHQQYFYKIP 19
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7; Conserv
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HPWAREHROWFTELP
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Pred. No.
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32;
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Maximum DB
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Perfect score:
      number of hits satisfying chosen parameters:
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116
1 REVIHPLATSHQQYFYKIPILV 22
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Listing first 45 summaries
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/cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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US-09-864-761-47234
US-09-747-835A-51
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2 US-10-312-312-51
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2 US-09-759-143-879
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US-09-895-879-879
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US-09-895-93-879
US-09-895-93-879
US-09-895-93-879
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Sequence 19, Appl
Sequence 19, Appl
Sequence 37, Appl
Sequence 47234, A
Sequence 50, Appl
Sequence 51, Appl
Sequence 51, Appl
Sequence 87, Appl
Sequence 879, App
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ALIGNMENTS

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APPLICANT: Raitano, Arthur B.

APPLICANT: Saffran, Douglas C.

APPLICANT: Mitchell, Steve Chappell

TITLE OF INVENTION: ANTIBODIES IMMUNOSPECIFIC FOR STEAP1 (AS

FILE REFERENCE: 511582001610

CURRENT APPLICATION NUMBER: US/10/011,095

CURRENT FILING DATE: 2001-12-06

PRIOR APPLICATION NUMBER: 09/323,873

PRIOR FILING DATE: 1999-06-01

PRIOR APPLICATION NUMBER: 60/087,520

PRIOR FILING DATE: 1998-06-01

PRIOR APPLICATION NUMBER: 60/091,183

PRIOR APPLICATION NUMBER: 60/091,183

PRIOR PILING DATE: 1998-06-30

NUMBER OF SEQ ID NOS: 32

SOPTWARE: FastSEQ for Windows Version 4.0

$580 ID NO 19
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                                                                                                                                                              US-10-011-095-19
                                                                             Query Match
Best Local S
Matches 22
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APPLICANT: Afar, Dan
APPLICANT: Hubert,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                               FEATURE:
OTHER INFORMATION: STEAP-1 peptide
                                                                                                                                                                                                                   LENGTH: 22
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                Similarity
                         REVIHPLATSHQQYFYKIPILV 22
REVIHPLATSHOOYFYKIPILV
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Leong, Kahan
                                                                             100.0%; Score 116; DB 14; ilarity 100.0%; Pred. No. 3.4e-11; Conservative 0; Mismatches 0;
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22
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US-10-165-044-37
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                                    PRIOR APPLICATION NUMBER: US 60/087,520
PRIOR FILLING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: US 60/091,183
PRIOR APPLICATION NUMBER: US 09/323,873
PRIOR APPLICATION NUMBER: US 09/323,873
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: US 09/455,486
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: WO 99/62941
PRIOR APPLICATION NUMBER: WO 99/62941
PRIOR FILING DATE: 1999-06-01
PRIOR FILING DATE: 1999-06-01
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SOFTWARE: FRASTSEQ for Windows Version
SEQ ID NO 19
LENGTH: 22
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19, Applica Publication No. US20 GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
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APPLICANT: Saffran, Douglas C.
APPLICANT: Mitchell, Steve Chappell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THE
                                                                                                                                                                                                                                                                                                                                         APPLICANT: Aya Jakobovits
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Agensys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/091,183 PRIOR FILING DATE: 1998-06-30
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                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/165,044
CURRENT FILING DATE: 2002-06-06
                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF FILE REFERENCE: 51158-20016.02
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity es 22; Conserv
FILING DATE:
                        APPLICATION NUMBER: PCT/US00/33040
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Leong, Kahan
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No. US20030055217A1
                                                                                                                                                                                                                                                                                                                                                                                                                                     Daniel E.H. Afar
Steven Chappell Mitchell
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                                                                                                                                                                                                                                                                                                                                                                                                                         Mary Faris
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  2000-12-06
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RESULT 4
US-09-864-761-47234
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; ORGANISM: Homo sapiens
US-10-165-044-37
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
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SOFTWARE: FASTSEQ for Windows
SEQ ID NO 37
LENGTH: 22
                                                              SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 47234
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                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
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PRIOR
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
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PRIOR
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CURRENT APPLICATION NUMBER: US/09/864,761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                          NUMBER OF SEQ ID NOS: 49117
                                                                                                                                 PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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PRIOR APPLICATION NUMBER: PCT/US01/00665
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                       LENGTH: 104
TYPE: PRT
ORGANISM: Homo sapiens
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APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US01/00661 FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                             FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US01/00668
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22; Conservative
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Chen, Wensheng
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1, David K.
                                                                                                                              2001-01-29
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RESULT 6
US-09-747-835A-51
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; ORGANISM: Homo sapiens
US-09-747-835A-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 09/729,739
PRIOR FILING DATE: 2000-12-04
PRIOR PELICATION NUMBER: US 09/653,450
PRIOR FILING DATE: 2000-08-31
PRIOR PELICATION NUMBER: US 09/620,312
PRIOR PELICATION NUMBER: US 09/620,312
PRIOR PELICATION NUMBER: US 09/598,042
PRIOR PELICATION NUMBER: US 09/598,042
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
                   Sequence 51, Application US/09747835A Patent No. US20020146692A1 GENERAL INFORMATION:
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Best Local :
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LENGTH: 267
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APPLICANT: Drmanac, Radoje T
APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIKE
TITLE OF INVENTION: LIKE) POLYPEPTIDES AND POLYNUCLEOTIDES
TILE REFERENCE: HYS-37CIP
CURRENT PEPLICATION NUMBER: US/09/747,835A
CURRENT FILING DATE: 2002-03-08
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APPLICANT: Yamazaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
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22; Conserv
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22; Conserv
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Zhang, --
Ten, Feiyan
Ten, Vinc
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Liu, Chenghua
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                                                                                                                                                              REVIHPLATSHOOYFYKIPILV 47
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                                                                                                                                                                                                                                        100.0%; Score 116; DB 9 llarity 100.0%; Pred. No. 5e-10; Conservative 0; Mismatches
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EXPRESSED IN LUNG, SIGNAL = 1.5

EXPRESSED IN FETAL LIVER, SIGNAL = 0.87

EXPRESSED IN ADULT LIVER, SIGNAL = 0.57

EXPRESSED IN BONE MARROW, SIGNAL = 0.59

SWISSPROT HIT: 067305, EVALUE 5.60e+00

EST_HUMAN HIT: BE875216.1, EVALUE 2.00e-54
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Pred. No. 1.8e-10;
; Mismatches 0;
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PRIOR FILLING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: US 09/653,450
PRIOR FILLING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US 09/620,312
PRIOR FILLING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US 09/598,042
PRIOR APPLICATION NUMBER: US 09/598,042
PRIOR PRILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR FILLING DATE: 2000-04-25
PRIOR FILLING DATE: 2000-04-25
                                                           PRIOR APPLICATION NUMBER: US 09/729,739
PRIOR FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: US 09/653,450
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US 09/620,312
PRIOR APPLICATION NUMBER: US 09/598,042
PRIOR APPLICATION NUMBER: US 09/598,042
PRIOR APPLICATION NUMBER: US 09/598,042
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APPLICANT: Zhang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: Drmanac, Radoje T
APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: METHODS AND
TITLE OF INVENTION: LIKE) POLY
FILE REFERENCE: HYS-37CIP
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO
TITLE OF INVENTION: LIKE) POLYPEPTIDES AND POLYNUCLEO
FILE REFERENCE: 21272-015-061/HYS-37CIP
CURRENT APPLICATION NUMBER: US/10/312,312
CURRENT FILING DATE: 2002-12-10
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CURRENT FILING DATE: 2002-03-08
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APPLICATION NUMBER: US 09/552,317
FILING DATE: 2000-04-25
APPLICATION NUMBER: US 09/488,725
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Tiu, Chenghua
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Ren, Feiyan
Asundi, Vinod
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Liu, Chenghua
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Wang, Dunrui
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US-09-759-143-879; Sequence 879, Application US/09759143; Patent No. US20020022248A1; GENERAL INFORMATION:
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                                                                                           RESULT 9
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PRIOR FILLING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US 09/620,312
PRIOR FILLING DATE: 2000-07-19
PRIOR PPLICATION NUMBER: US 09/598,042
PRIOR PILLING DATE: 2000-06-20
PRIOR PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR FILLING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILLING DATE: 2000-01-21
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Best Local Similarity
Matches 22; Conserv
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LENGTH: 267
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: Drmanac, Radoje T
APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIKE
TITLE OF INVENTION: LIKE) POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: 21272-015-061/HYS-37CIP
CURRENT FAPLICATION NUMBER: US/10/312,312
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: US 09/729,739
PRIOR FILING DATE: 2000-12-04
PRIOR FILING DATE: 2000-12-04
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NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn version 3.0
SEQ ID NO 50
                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 63
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ORGANISM: Homo sapiens
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22; Conserv
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Wang, Dunrui
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Liu, Chenghua
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Ren, Feiyan
                                                                                                                                                                                                                         100.0%; Score 116; DB 1. ilarity 100.0%; Pred. No. 5e-10; Conservative 0; Mismatches
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APPLICANT: MCNeill, Patricia D.
APPLICANT: HOUGHTON, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TH
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION UNMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 879
LENGTH: 339
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US-09-780-669-879
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APPLICANT: Xu, Jia
APPLICANT: Dillon,
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CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
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TYPE: PRT
ORGANISM: Homo sapiens
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TYPE: PRT
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US20020051977A1
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                                                                                                                                                                                                                                                                                         Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
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Hepler, William
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Kalos, Michael D.
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Carter, Darrick
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Mitcham, Jennifer L.
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Carter, Darrick
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Kalos, Michael
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ick, Thomas S.
                                                                                                                                                                                           John
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; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020187472A1 g6572948
US-09-802-520-11
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US-09-802-520-11
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US-09-822-827-879
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                                                                                                                                                                                                    SOFTWARE: PEI
SEQ ID NO 11
LENGTH: 339
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Best Local
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/802,520
CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C1
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lal,
                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: STEAP-RELATED PROTEIN FILE REFERENCE: PC-0037 US
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                                                                                                                                                                        ORGANISM: Homo sapiens
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                                                                     Similarity
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Chen, Huei-Mei
Ison, Craig H.
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Pred. No. 6.5e-10;
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Pred. No. 6.5e-10;
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Pred. No. 6.5e-10;
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 879
LENGTH: 339
TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT:
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CURRENT FILING DATE: 2001-06-29
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.534C2
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Ter, Darrick
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Mitcham, Jennifer L.
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Vinals de Bassols, Carlota
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Hepler, William T.
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McNeill, Patricia D. Houghton, Raymond L.
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                                         Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
                                                                                                                                                                  Retter, Marc W. Stolk, John A.
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Kalos, Michael D.
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                              Hural, John
                                                                                       Wang, Aijun
                                                                                                                     Vedvick, Thomas
Carter, Darrick
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                                                                                                        Samuel X.
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100.0%; Pred. No. 6.5e-10;
tive 0; Mismatches 0;
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RESULT 15

US-10-205-267-13

Sequence 13, Application US/10205267

Publication No. US20030064397A1

GENERAL INFORMATION:
APPLICANT: Spancake, Kimberly M.
APPLICANT: Rickert Paula K.
APPLICANT: Ison, Craig H.
APPLICANT: Ison, Craig H.
FIILE OF INVENTION: TRANSMEMBRANE PROTEIN DIFFERENTIALLY EXPRESSED IN PROSTATE AND LUTITLE OF INVENTION: TUMORS

FILE REFERENCE: PV-0008 CIP
CURRENT APPLICATION NUMBER: US/10/205,267

CURRENT FILING DATE: 2002-07-24

NUMBER OF SEQ ID NOS: 13

SOUTMARE: PERL Program

SEQ ID NO 13

LENGTH: 339
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APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
INTIE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
ITITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C26
CURRENT FILLOATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 879
LENGTH: 339
TYDE: DRT
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; ORGANISM:
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank ID No: 96572948
US-10-205-267-13
Search completed: July 12, 2004, 14:27:49 Job time : 39.8837 secs
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Best Local Similarity
Matches 22; Conserv
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                                                                                 92 REVIHPLATSHOOYFYKIPILV 113
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2: /cgn2_6/ptodatta/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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(c) 1993 - 2004 Compugen Ltd
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US-09-489-039A-8972
US-09-357-251-24
US-09-357-251-24
US-09-134-010C-3888
US-09-134-010C-3888
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US-09-012-504A-12
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US-09-012-504A-12
US-09-012-504A-12
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27, Appl
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23, Appl
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26, Appl
27, Appl
28, Appl
29, Appl
20, Ap
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Query Match Best Local Similarity Matches 22; Conser Matches 1 REVIHPLAT Qy 1 REVIHPLAT Db 1 REVIHPLAT	APPLICATION FILLING DATE: R OF SEQ ID NO 19 TH: 22 FAT UNES: ARTIFICATION R INFORMATION R INFORMATION R INFORMATION	APPLICANT: Daniel B. Afar APPLICANT: Rene S. Hubert APPLICANT: Rene S. Hubert APPLICANT: Arthur B. Rait APPLICANT: Arthur B. Rait APPLICANT: Douglas C. Saf APPLICANT: Steve Chappell TITLE OF INVENTION: NOVEL TITLE OF INVENTION: EXPRE- FILE REFERENCE: 129.16USU2 CURRENT APPLICATION NUMBER: CURRENT FILING DATE: 1999 PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER:	RESULT 1 US-09-323-873A-19 (F. Sequence 19, Applic Fratent NO. 6329503	28 41 35.3 30 41 35.3 30 41 35.3 31 41 35.3 32 41 35.3 33 41 35.3 34 41 35.3 36 41 35.3 36 41 35.3 37 41 35.3 36 41 35.3 37 41 35.3 38 40 31 35.3 36 41 35.3 37 41 35.3 38 40 31.3 37 41 35.3 38 40 31.3 39 40 31.3 39 40 31.5 39 40 31.5 31 31 31 31 31 31 31 31 31 31 31 31 31 3
100.0%; Score 116; DB 4; L 100.0%; Pred. No. 6.7e-12; vative 0; Mismatches 0; SHQQYFYKIPILV 22 	4 14	E. Afar Hubert Leong B. Raitano B. Raitano B. Raitano Chappell Mitchell NOVEL SERPENTINE TRANSMEMBRANE EXPRESSED IN HUMAN CANCERS AND 9.16USU2 N NUMBER: US/09/323,873A E: 199-06-01 NUMBER: 60/087,520	ALIGNMENTS 19 Application US/09323873A MATION:	396 3 US-09-461-474-2 592 2 US-08-366-490-2 592 3 US-08-860-483A-2 879 1 US-08-220-151-2 879 1 US-08-220-151-3 879 1 US-08-413-118-3 879 1 US-08-413-118-3 879 1 US-08-413-118-3 879 1 US-08-413-118-3 879 1 US-08-473-446-2 879 3 US-08-473-446-3 879 3 US-08-173-446-3 879 3 US-08-173-446-3 879 3 US-08-173-426-3 879 3 US-09-107-532A-4856 68 4 US-09-134-001C-8858 77 4 US-09-134-001C-8858 77 4 US-09-134-001C-8858 77 4 US-09-219-79-2 303 1 US-08-219-79-2 303 1 US-08-219-79-2 304 US-09-219-79-2
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Sequence 2, Application US/09323873A
Patent No. 6329503
GENERAL INFORMATION:
APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Kahan Leong
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Steve Chappell Mitchell

RESULT 2 US-09-323-873A-2

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US-09-134-001C-3548
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-685-166A-879
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US-09-685-166A-879
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Sequence 3548, Application US/09134001C
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Best Local Similarity
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C21
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
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ORGANISM: Homo Sapiens
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Dillon, Davin C.
Mitcham, Jennifer L.
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Pred. No. 1.4e-10;
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Pred. No. 1.4e-10;
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US-08-682-847-2
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PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3548
    Query Match
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                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                         APPLICATION NUMBER: US/08/682,847
FILING DATE: 12-UUL-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: PARK, FREDDIE K.
REGISTRATION NUMBER: 35.636
REFERENCE/DOCKET NUMBER: 29310-200
                                                  MOLECULE TYPE:
                                                                                                                                                                            TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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ADDRESSEE: MORRISON
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                                                                 TYPE: am TOPOLOGY:
                                                                                                                                             TELEFAX: (41)
TELEX: 70614
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                                                                                                933 amino acids
                                                                                                                                                             (415) 494-0792
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VAN DEN HURK, SYLVIA
                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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 Score 44;
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Pred. No.
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Length 933;
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US-09-252-991A-25798
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                                           RESULT 8
US-09-134-000C-4003
                                                                                                                                                                                                                                       ; ORGANISM: Klebsiella pneumoniae US-09-489-039A-8972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25798, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8972, Application US/09489039A Patent No. 6610836
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             Sequence 4003, Application US/09134000C Patent No. 6617156
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SEQ ID NO 8972
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Best Local
GENERAL INFORMATION
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE:
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TYPE: PRT
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                                                                                                                                                                                                                                                                                          LENGTH: 245
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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46.2%;
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Pred. No. 43;
3; Mismatches
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                                                                                                                                         HQQYFYKIP 19
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Pred. No.
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              APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO AC TITLE OF INVENTION: BEDIERMIDIS FOR DIAGNOST FILE REFERENCE: GTC-007 EPIDERMIDIS FOR DIAGNOST CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                       ; Sequence 3888, Application US/09134001C ; Patent No. 6380370 ; GENERAL INFORMATION:
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PRIOR FILING DATE: 1997-08-15
NUMBER OF SEO ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEO ID NO 4003
LENGTH: 220
TYPE: PRT
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SEQ ID NO 24
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Patent No.
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Best Local
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APPLICANT: Schwaber, James S.
APPLICANT: Schwaber, James S.
TITLE OF INVENTION: Plant Aminoacyl-tRNA Synthetase
FILE REFERENCE: BB-1193
CURRENT APPLICATION NUMBER: US/09/357,251
CURRENT FILING DATE: 1999-07-20
EARLIER APPLICATION NUMBER: 60/93,530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Falco, S. Carl
APPLICANT: Famodu, Layo O.
APPLICANT: Orozco, Buddy
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CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
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NUMBER OF SEQ ID NOS: 37
NUMBER OF
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Local Similarity 41.2%;
les 7; Conservarium
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o. 6271441
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SEQ ID NOS: 5674
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Pred. No.
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Pred. No.
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                                                                                                                                                    AMINO ACID SEQUENCES RELATING DIAGNOSTICS AND THERAPEUTICS
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US-08-471-112A-4
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       Matches
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LENGTH: 319
                                         Query Match
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Best Local Similarity 47.1%; Pred. No.
Matches 8; Conservative 1; Mismatc
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/384,524
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/312,023
FILING DATE: 26-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/207,975
FILING DATE: 08-MAR-1994
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                   TELEFAX: 202-408-4400 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
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                                                                                           TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                NAME: Siekman, Michael T.
REGISTRATION NUMBER: 36,276
REFERENCE/DOCKET NUMBER: 01142.0058-00000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: EFFECTOR PROTEINS OF RAPAMYCIN
NUMBER OF SEQUENCES: 23
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   Local Similarity hes 8; Conserv
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TO TO NO:
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STREET: 1300 I Street, N.W.
                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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ilarity 50.0%;
Conservative
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Score 42; DB 4; Le
Pred. No. 2.8e+02;
2; Mismatches 6;
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                                   Length 1140;
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RESULT 13
US-08-360-144A-12
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US-09-012-515A-12
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                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 617-832-7000 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/360
FILING DATE: 20-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: APV-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT STREET: One Post Office Square
                                                                          APPLICANT: Berlin, Vivian
APPLICANT: Chiu, Maria Isabel
APPLICANT: Cottarel, Guillaume
APPLICANT: Damagnez, Veronique
TITLE OF INVENTION: IMMUNOSUPPRESSANT TARGET PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1809 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,515A
FILING DATE:
                                                              NUMBER OF SEQUENCES:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cottarel, Guillaume APPLICANT: Damagnez, Veronique TITLE OF INVENTION: IMMUNOSUPPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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ADDRESSEE: FOLEY, HOAG & ELIOT STREET: One Post Office Square
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Local Similarity 50.0%;
hes 8; Conservative
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ZIP: 02109-2170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
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Pred. No. 4.7e+02;
2; Mismatches 6;
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

02109-2170

USA

Boston: MA

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GENERAL INFORMATION:

APPLICANT: Berlin, V.

APPLICANT: Chiu, I.

APPLICANT: Chiu, I.

APPLICANT: Chiu, I.

APPLICANT: Cottarel, G.

APPLICANT: Cottarel, G.

FILE OF INVENTION: IMMUNOSUPPRESSANT TARGET PROTEINS

FILE REFERENCE: APBL-05-036

CURRENT APPLICATION NUMBER: US/09/012,504A

CURRENT FILING DATE: 1998-01-33

PRIOR APPLICATION NUMBER: 08/360,144

PRIOR FILING DATE: 1994-12-20

PRIOR FILING DATE: 1994-05-27

PRIOR FILING DATE: 1994-05-27

PRIOR FILING DATE: 1994-05-27

PRIOR FILING DATE: 1994-05-27
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RESULT 15
US-09-012-399A-12
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                                                                                                                                              Matches
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SEQ ID NO 12
LENGTH: 1809
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Patent No. 6464974
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                                                                                                                                                             Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1809 amino aci
                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: 17-832-1000
TELEPHONE: 617-832-7000
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APPLICATION UMBER: US/08/360,144A
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y mducn 36.2%; Score 42; DB 3; Local Similarity 50.0%; Pred. No. 4.7e+02; les 8; Conservative 2. Micmati.
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REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: APV-036.02
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OPERATING SYSTEM: PC-DOS/MS-DOS
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Pred. No.
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Search completed: July 12, 2004, 14:12:23 Job time: 13.5581 secs
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                                                                                                                                                Matches
                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/360,144
FILING DATE: 20-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REGISTRATION NUMBER: APV-036.02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Betlin, Vivian
APPLICANT: Chiu, Maria Isabel
APPLICANT: Cottarel, Guillaume
APPLICANT: Damagnez, Veronique
TITLE OF INVENTION: INMUNOSUPPRESSANT TARGET PROTEINS
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 617-832-100
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 617-832-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/012,399A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                            Local Similarity
nes 8; Conserv
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 02109-2170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                          943
                                                                                                           1 REVIHPLATSHQQYFY 16
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                                                                                                                                                                  36.2%;
                                                                          958
                                                                                                                                                                  Score 42; DB 4; 1
Pred. No. 4.7e+02;
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                                                                                                                                                  Mismatches
                                                                                                                                                                                     Length 1809;
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A_Geneseq_29Jan04:*
1: geneseqp1980s:*
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length: 2000000000
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128.567 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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116
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                geneseqp2003as:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	00	7	9	σı	4	w	2	μ.	No.	Result
116	116	116	116	116	116	116	116	116	116	116	116	116	116	116	116	116	116	116	116	116	116	116	116	116	Score	
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258	258	258	258	258	258	258	258	258	258	258	258	258	258	258	255	255	254	254	104	104	104	104	22	22		
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ABU98386	ABU98388	ABU98394	ABU98397	ABU98396	ABU98431	ABU98384	ABU98391	ABU98390	ABU98393	ABU98387	ABU98392	ABU98424	ABU98389	ABU98395	ABU98428	ABU98429	ABU98425	ABU98426	ABG43832	ABG55696	AAM73944	ABB40417	AAE02786	AAY58198	i	
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45	44	43	42	41	40	39	38	37	36	35	υ 4	υ U	32	31	30	29	28	27	26
116	116	116	116	116	116	116	116	116	116	116	116	116	116	116	116	116	116	116	116
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0		100.0	100.0
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ADB75573	ABU63313	ABR54499	ABU98430	ABU98414	ABU98383	ABG61813	ABB95387	ABU71818	AAM78845	AAU69927	AAM01282	AAY58194	ABU98385	ABU98427	ABU98432	ABU60887	ABU60886	ABU98398	ABU98399
Adb75573	Abu63313	Abr54499	Abu98430	Abu98414	Abu98383	Abg61813	Abb95387	Abu71818	Aam78845	Aau69927	Aam01282	Aay58194	Abu98385	Abu98427	Abu98432	Abu60887	Abu60886	Abu98398	Abu98399
Prostate	Human six	Prostate	STEAP-1 V	STEAP-1 v	Novel hum	Prostate	Human P78	Prostate	Human pro	Human pro	P789P ami	Human STR	Novel hum	STEAP-1 V	STEAP-1 V	Human G p	Human G p	Novel hum	Novel hum

ALIGNMENTS

AAY58198 standard; peptide; 22 ₽Ā

AAY58198;

14-MAR-2000 (first entry)

Human STRAP-1 peptide, corresponding to STRAP-1 extracellular region 1.

AAY5819A 14-M
AAY59A AAY5
XX AAY5
XX AAY5
XX AAY5
XX AAY5
XX Huma
XX Serp
XW Pros
XW Huma
XX Serp
XW Huma
XX Homoni
XW Pros
XX Homoni
XW Homon Serpentine transmembrane antigen of the prostate; STRAP-1; prostate; transmembrane domain; type IIIa membrane protein; expression; cancer; prostate cancer; bladder cancer; colon cancer; pancreatic cancer; ovarian cancer; tumour antigen; immunisation; immune response; cellular; humoral; anticancer vaccine; antibody; detection; diagnosis; prognosis; monitoring; susceptibility; therapeutic inhibitor; drug targetting; recombinant protein.

Synthetic.

Homo sapiens.

09-DEC-1999.

W09962941-A2

01-JUN-1999; 99WO-US012157.

01-JUN-1998; 30-JUN-1998; 98US-0087520P. 98US-0091183P.

(UROG-) (AFAR/) (HUBE/) (LEON/) (RAIT/) (SAFF/) AFAR D E. HUBERT R S. UROGENESYS INC.

Afar DE, LEONG K.
RAITANO A B.
SAFFRAN D C. Hubert RS, Leong χ, Raitano ĂΒ, Saffran

DC;

WPI; 2000-072832/06.

Novel proteins useful as diagnostic markers particularly for prostatic cancer. and therapeutic targets,

Disclosure; Page 22; 83pp; English

Sequences AAY58198-Y58200 represent synthetic peptides that correspond the extracellular regions of STRAP-1 (serpentine transmembrane antigen off o

the prostate, AAY58194). These peptides were used to raise monoclonal anti-STRAP-1 antibodies. STRAP-1 is the prototype member of the STRAP family of proteins (AAY58194-Y58197) which exhibit a high degree of

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AABO2786
ID AABO
XX AABO
AC AAEO
DT 06-A
XX Huma
KW Six
KW chro
KW covar
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W Ovar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cc structural conservation, but which show no significant structural conservation, but which show no significant structural cc chromosome 7p22. STRAP-1 is thought to be a type IIIa membrane protein cc and is expressed predominantly in prostate cells in normal human tissues. Structurally, STRAP-1 is a 339 amino acid protein characterised by six transmembrane domains and intracellular N- and C-termini, suggesting that it folds in a "sexpentine" manner into three extracellular and two cc intracellular loops. STRAP-1 mRNA and protein expression is maintained at high levels and throughout all stages of prostate cancer. STRAP-1 mRNA cr and/or protein is also overexpressed in certain other cancers, including bladder, colon, pancreatic and ovarian cancer. The function of the STRAP proteins is not known. They may be ion channels (from the presence of six transmembrane domains, a feature which is shared by certain ion channels) or gap-junction proteins (from immunhistochemical staining). STRAP-1 and STRAP are cell-surface tumour antigens. Immunisation with a STRAP capenessing cells. STRAP proteins may be used to identify specific-binding agents, to produce anticoncer vaccines and to generate specific monitoring of cancers (or susceptibility to cancer), as therapeutic cancer nucleic acids may be used for detection, prognosis, and concleic acids may be used for identifying STRAP-expressing cells created in the cell surface, they are easily targetted by systemically administered agents. For identifying STRAP-expressing cells for screening inhibitors of STRAP expression and for therapeutic on prostatic epithelial cells, agents targetted to them should have minimal side effects on other tissues
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    Afar DEH,
Faris M, J
                                                                                                                                                                                                                                                                                                                                                       Human; cytostatic; antiproliferative; vaccine; gene therapy; six transmembrane epithelial antigen of the prostate-1; STEAP-1; chromosome 7p22.3; cancer; prostate; colon; bladder; pancreatic; lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE02786 standard; peptide;
                                                                                                                         06-DEC-1999;
                                                                                                                                                                         06-DEC-2000; 2000WO-US033040
                                                                                                                                                                                                                          07-JUN-2001
                                                                                                                                                                                                                                                                       WO200140276-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE02786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                          (UROG-) UROGENESYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   بـــر
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REVIHPLATSHQQYFYKIPILV 22
    Hubert RS,
Jakobovits A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVIHPLATSHOOYFYKIPILV 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   loop
                                                                                                                            99US-00455486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #1 of human STEAP-1, suitable for cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                             Raitano AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 116; DB 3;
Pred. No. 1.4e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                           Saffran DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 22;
                             Mitchell SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   into pFc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Дb

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RESULT 3
ABB40417
ID ABB4
XX ABB4
XX ABB4
XX Huma
AC ABB4
XX Huma
XX Huma
XX Huma
XX Homc
PN WO20
XX HOMC
PN WO21
PP 30--1
PR 30--1
PR 31--1
PR 21--1
PR 31--1
PR 31-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           comparises administering a vaccine composition to the patient. CC comprises administering a vaccine composition to the patient. Treating a patient with a cancer that expresses STEAP, or inhibiting growth or killing cells expressing STEAP in a patient. CC patient with a cancer that expresses STEAP, or inhibiting growth or killing cells expressing STEAP, composition to the patient. Treating a composition to the patient and comparises administering to the patient a comparise composition to the patient a comparise that comprises the comparise that the variable domains of the heavy and light chains of the monoclonal antibody that comprises the comparise that the vactor delivers the comparise that the vactor delivers the comparise that the vactor delivers the congle chain monoclonal antibody coding sequence to the cancer cells and the encoded single chain monoclonal antibody is expressed intracellularly. The present sequence is extracellular loop of STEAP-1 comparison is located on chromosome 7p22.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                             04-FEB-2000; 2000US-0180312P, 26-MAY-2000; 2000US-0207456P, 30-UUN-2000; 2000US-0068408, 03-AUG-2000; 2000US-0234687P, 21-SEP-2000; 2000US-0234687P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; foetal liver; gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB40417 standard; peptide; 104
                                                             WPI; 2001-483447/52.
                                                                                                                                                                                                                                                      04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US000669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide #7923 encoded by human foetal liver single exon probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB40417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 22 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to human six transmembrane epithelial antigen of the prostate (STEAP) protein. STEAP is a member of cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New STEAP (six transmembrane epithelial antigen of the prostate) proteins, expressed in human cancers, useful for detecting and treating
                                                                                                                                                                                                                                                                                      27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              surface serpentine transmembrane antigens. STEAP gene is used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 19; Page 102; 187pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-367804/38.
                                                                                                                                                                                        (MOLE-)
                                                                                                                              SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                        MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REVIHPLATSHOOYFYKIPILV 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REVIHPLATSHOOVEYKIPILV 22
                                                                                                                           Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                   2000US-0236359P.
2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                           Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 116; DB 4;
Pred. No. 1.4e-11;
                                                                                                                           Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single exon nucleic acid probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Human genome-derived single exon nucleic acid probes useful for analyzing

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RESULT 4
AAM73944
ID AAM7
XX AAM7
AX A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human bone marrow expressed probe encoded
                                                                                                                                                                                                                                                                                        Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US000668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200157276-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM73944 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-)
                                                                                                                                                                  present
                                                                                                                   marrow.
                                                                                                                                                                                                                                                                                                                                    2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                 SG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression
                                                                                                                                                                                                                                                               expression
                                                                                                                                                                                                                                                             genome-derived single exon nucleic acid probes useful for analyzing expression in human bone marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27; SEQ
                                                                                                                                            which are derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         μ
                                            encoded by
                                                                         lymphoma,
                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                    row. They can be used to measure gene expression in bone marrow which may enable the improved diagnosis and treatment of cance: lymphoma, leukaemia and myeloma. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REVIHPLATSHQQYFYKIPILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVIHPLATSHOOYFYKIPILV
                                                                                                                                                                                                                                                                                                                                                                                 Hanzel
                                                                                                                                                                                                                 SEQ ID
                                                                                                                                                                  invention provides a number of single exon nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0207456P
2000US-00608408
2000US-00632366
2000US-023468P
2000US-023468P
2000US-0236359P
2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0180312P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ħ.
                                                                                                                                                                                                                                                                                                                                                                              DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NO
                                                                                                                                                                                                            NO 34250; 658pp + Sequence Listing;
                                              one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expressed exon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33052; 639pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                 Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fetal liver.
                                                                                                                                            from
                                                                                                                                                                                                                                                                                                                                                                              ξ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 116; DB 4;
Pred. No. 7.4e-11;
                                                                                                                                         genomic sequences expressed
                                                                                                                                                                                                                                                                                                                                                                                 Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lymphoma; myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                              English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104;
                                                                                                                                            in the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Sequence 104 AA

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REVIHPLATSHQQYFYKIPILV

REVIHPLATSHOOYFYKIPILV

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RESULT 5
ABG55696
Query Match
Best Local S
Matches 22
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Best Local S
Matches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-02346359.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Penn
                                                                           Sequence
                                                                                                         associated with coronary heart disease. ABG47348-ABG59930 r liver single exon encoded peptides of the invention. Note: information for this patent does not appear in the printed but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                   measuring human gene expression in a sample derived from human adultiver, comprising one of 13109 defined nucleotide sequences given i specification (or complements/ fragments). The probe hybridises at
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human liver peptide,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG55696
                                                                                                                                                                                       involved in genetic liver diseases such as cirrhosis,
hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
associated with coronary heart disease. ABG47348-ABG59930 represent human
                                                                                                                                                                                                                                           stringency to a nucleic acid molecule expressed in the human adult liver (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be
                                                                                                                                                                                                                                                                                                                                             The invention relates to a single exon nucleic acid probe (SENP) measuring human gene expression in a sample derived from human a
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ilarity 100.0%;
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Pred. No. 7.4e-11;
Score 116; DB 4;
Pred. No. 7.4e-11;
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                                   Length 104;
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XXX PR 30-J
PR 26-M
PR 30-J
PR 21-S

Complements of the 1230 open remarked traines between the movel set of probes. Also included are a microarray comprising the novel set of probes call the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample collection of detectably labeled nucleic acids derived from human lung comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the carray; identifying exons in a eukaryotic genome, comprising (a) contacting the each probe of the eukaryote; and (b) detecting specific hybridisation of detectably collection acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single exon probe, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single comprising one of 12011 sequences, mentioned in the specification, or encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spatially-addressable set of single exon nucleic acid probes, used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-114183/15
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                       The invention describes a composition comprising a substance that modulates the status of a protein (I) of 340 or 283 amino acids, or of any of the 15 sequences of 259 amino acids, given in the specification, or a molecule that is modulated by the protein, where the status of the cell that expresses the protein is modulated. The compositions, proteins, polynucleotides and methods are useful for treating and detecting cancer. The STEAP-1-related proteins are useful for generating cancer vaccines. The polynucleotides are useful as tools for delineating, with greater precision, cytogenetic abnormalities in the chromosomal region that encodes STEAP-1 that may contribute to the malignant phenotype. This is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STEAP-1; six transmembrane epithelial antigen of the prostate; caccer vaccine; delineation; cytogenetic abnormality; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                           STEAP-1-related protein,
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05-APR-2002; 2002US-0370387P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            composition comprising a substance that modulates the status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REVIHPLATSHQQYFYKIPILV 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ge
                                                                                                                                                                                                                                                                                                                                                                                Page 169-170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ξ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Raitano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for treating
                                                                                                                                                                                                                                                                                                                                                                          248pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0:
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Pred. No. 7.4e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Challita-Eid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ΡM,
                                                                                                                                                                                                                                                                                                                                                                                                                                           and detecting cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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acid sequence of a variant

of human six transmembrane

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ABU98425
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                                                                Query Match
Best Local
                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                    The invention describes a composition comprising a substance that modulates the status of a protein (I) of 340 or 283 amino acids, or of any of the 15 sequences of 259 amino acids, given in the specification, or a molecule that is modulated by the protein, where the status of the cell that expresses the protein is modulated. The compositions, proteins, polymucleotides and methods are useful for treating and detecting cancer. The STEAP-1-related proteins are useful for generating cancer vaccines. The polymucleotides are useful as tools for delineating, with greater precision, cytogenetic abnormalities in the chromosomal region that encodes STEAP-1 that may contribute to the malignant phenotype. This is the amino acid sequence of a variant of human six transmembrane epithelial antigen of the prostate or STEAP-1
                                                                                                    Sequence
                                                                                                                                                                                                                                                                                           Example 53; Page 169-170;
                                                                                                                                                                                                                                                                                                                     New composition STEAP-1-related
                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-313240/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                   06-SEP-2001;
05-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-SEP-2002; 2002WO-US028371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STEAP-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STEAP-1 variant 8P1D4 v.1 #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003022995-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU98425 standard; protein; 254 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 254 AA;
                                                                                                                                                                                                                                                                                                                                                                                                           (AGEN-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  epithelial antigen
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                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                           AGENSYS
                   REVIHPLATSHQQYFYKIPILV 22
                                                                                                    254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     six transmembrane epithelial antigen of the prostate; ca accine; delineation; cytogenetic abnormality; cytostatic;
REVIHPLATSHQQYFYKIPILV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REVIHPLATSHOOYFYKIPILV 113
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                                                                                                                                                                                                                                                                                                                                                                                  Ge W,
                                               100.0%; s
llarity 100.0%; I
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                    AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                   2001US-0317840P.
2002US-0370387P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                   comprising a substance protein, useful for tre
                                                                                                                                                                                                                                                                                                                                                                                  Raitano AB,
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                                                                                                                                                                                                                                                                                           248pp; English.
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                                               Score 116; DB 6
Pred. No. 2e-10;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                Challita-Eid PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 116; DB 6
Pred. No. 2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                 treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STEAP-1
                                                                                                                                                                                                                                                                                                                             that modulates the status of
                                                                        6
                                                                                                                                                                                                                                                                                                                and detecting cancer.
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                                                                                                                                                                                                                                                                                                                                                                                 Jakobovits
                                                                       Length 254;
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                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer;
                                               Gaps
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ABU98429
                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                  Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                             The invention describes a composition comprising a substance that modulates the status of a protein (I) of 340 or 283 amino acids, or of any of the 15 sequences of 259 amino acids, given in the specification, or a molecule that is modulated by the protein, where the status of the cell that expresses the protein is modulated. The compositions, proteins, polymucleotides and methods are useful for treating and detecting cancer. The STEAP-1-related proteins are useful for generating cancer vaccines. The polymucleotides are useful as tools for delineating, with greater precision, cytogenetic abnormalities in the chromosomal region that encodes STEAP-1 that may contribute to the malignant phenotype. This is the amino acid sequence of a variant of human six transmembrane epithelial antigen of the prostate or STEAP-1
     STEAP-1; six transmembrane epithelial antigen of the prostate; cancer; cancer vaccine; delineation; cytogenetic abnormality; cytostatic;
                                                                                                                               ABU98428
                                                                                                                                                                                                                                                                                                          Sequence 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 53; Page 172; 248pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New composition comprising a substance that modulates the status of a STEAP-1-related protein, useful for treating and detecting cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-313240/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-SEP-2001;
05-APR-2002;
                                                  STEAP-1
                                                                           31-JUL-2003
                                                                                                        ABU98428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Faris M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-SEP-2002; 2002WO-US028371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STEAP-1; six transmembrane epithelial antigen of the prostate; cancer; cancer vaccine; delineation; cytogenetic abnormality; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STEAP-1 variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABU98429 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine.
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                                                                                                                                                                                                  92
                                                                                                                                                                                                                                                    22;
                                                                                                                                                                                                                        1 REVIHPLATSHQQYFYKIPILV
                                                 variant 8P1D4 v.2
                                                                                                                                                                                                                                                                    Similarity
                                                                                                                               standard; protein;
                                                                                                                                                                                                  REVIHPLATSHOOYFYKIPILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ge W,
                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001US-0317840P
2002US-0370387P
                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Raitano AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein;
                                                                                                                                                                                                                                                                 100.0%;
                                                 #3
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                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                               Score 116; DB 6
Pred. No. 2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Challita-Eid PM,
                                                                                                                                                                                                  113
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                                                                                                                               A
                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                               DB 6;
                                                                                                                                                                                                                                                    0
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                                                                                                                                                                                                                                                                            Length 255;
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vaccine

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RESULT 11
ABU98395
ID ABU98
XX ABU98
XX ABU98
XX ABU98
XX STEAF
KW CANCE
KW CANCE
KW VACCI
XX WO200
XX WO200
XX WO200
XX O6-SI
PR 06-SI
PR 06-SI
PR 06-SI
PR 06-SI
PR (AGE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes a composition comprising a substance that modulates the status of a protein (I) of 340 or 283 amino acids, or of any of the 15 sequences of 259 amino acids, given in the specification, or a molecule that is modulated by the protein, where the status of the cell that expresses the protein is modulated. The compositions, proteins, polynucleotides and methods are useful for treating and detecting cancer. The STEAP-1-related proteins are useful for generating cancer vaccines. The polynucleotides are useful as tools for delineating, with greater precision, cytogenetic abnormalities in the chromosomal region that encodes STEAP-1 that may contribute to the malignant phenotype. This is the chromosomal region that the chromosomal region that the chromosomal region that the substant of human six transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 255 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New composition comprising a substance that modulates the status of a STEAP-1-related protein, useful for treating and detecting cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-SEP-2001; 2001US-0317840P.
05-APR-2002; 2002US-0370387P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                              06-SEP-2001; 2001US-0317840P.
05-APR-2002; 2002US-0370387P.
                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                           STEAP-1; six transmembrane epithelial antigen of the prostate; ca cancer vaccine; delineation; cytogenetic abnormality; cytostatic;
                                                                                                                                                                                                                                                     Novel human gene STEAP-1 variant 13.
                                                                                                                                                                                                                                                                                    31-JUL-2003
                                                                                                                                                                                                                                                                                                                                             ABU98395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   epithelial antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-MAR-2003
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                                                                          06-SEP-2002; 2002WO-US028371
                                                                                                        20-MAR-2003
                                                                                                                                    WO2003022995-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AGEN-) AGENSYS INC.
   (AGEN-) AGENSYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      REVIHPLATSHOOYFYKIPILV 22
                                                                                                                                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                                                                                                     REVIHPLATSHOOVEYKIPILV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ge W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Raitano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the prostate or STEAP-1
                                                                                                                                                                                                                                                                                                                                           protein; 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 116; DB 6
Pred. No. 2e-10;
Mismatches
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                                                                                                                                                                                                                                                                                                                                              A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             255;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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ARBSULT 12
ABU98389
ID ABU988
XX ABU98
XX ABU98
XX STEAP
KW Cance
KW Vacci
XX Vacci
XX WO200
XX WO200
XX WO200
XX WO5-AP
PR 05-AP
XX (AGEN
XX WPI;
DR N-PSD
XX WPF
PT STEAP
XX New C
PT STEAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes a composition comprising a substance that modulates the status of a protein (I) of 340 or 283 amino acids, or of any of the 15 sequences of 259 amino acids, given in the specification, or a molecule that is modulated by the protein, where the status of the cell that expresses the protein is modulated. The compositions, proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encodes STEAP-1 that may contribute to the malignant phenotype. the amino acid sequence of a variant of human six transmembrane epithelial antigen of the prostate or STEAP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polynucleotides and methods are useful for treating and detecting cancer. The STEAP-1-related proteins are useful for generating cancer vaccines. The polynucleotides are useful as tools for delineating, with greater precision, cytogenetic abnormalities in the chromosomal region that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New composition comprising a substance that modulates the status STEAP-1-related protein, useful for treating and detecting cancer
                                                        New composition comprising a substance that STEAP-1-related protein, useful for treating
                                                                                                                                              Faris M,
                                                                                                                                                                                                      06-SEP-2001;
05-APR-2002;
                                                                                                                                                                                                                                                 06-SEP-2002; 2002WO-US028371.
                                                                                                                                                                                                                                                                               20-MAR-2003
                                                                                                                                                                                                                                                                                                         WO2003022995-A2
                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                   vaccine.
                                                                                                                                                                                                                                                                                                                                                                               STEAP-1; six transmembrane epithelial antigen of the prostate; cancer; cancer vaccine; delineation; cytogenetic abnormality; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human gene STEAP-1 variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU98389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU98389 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Fig 2M; 248pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Faris M,
The invention describes a composition comprising
                            Example 2; Fig 2G; 248pp; English
                                                                                                     N-PSDB;
                                                                                                                                                                           (AGEN-) AGENSYS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                 2003-313240/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
22; Conserv
                                                                                                     ACD02603.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACD02609
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                                                                                                                                              Ge W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                      2001US-0317840P
2002US-0370387P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ξ
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                                                                                                                                                AB,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 116; DB 6
Pred. No. 2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Challita-Eid PM,
                                                                                                                                                Challita-Eid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                         treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6;
                                                                                                                                                PM,
                                                                        modulates the status of
                                                           and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jakobovits
                                                                                                                                                 Jakobovits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 258;
 ø
                                                         detecting
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   substance that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer.
                                                           cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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RESULT 13
ABU98424
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Best Local
     The invention describes a composition comprising a substance that modulates the status of a protein (I) of 340 or 283 amino acids, or of any of the 15 sequences of 259 amino acids, given in the specification, or a molecule that is modulated by the protein, where the status of the cell that expresses the protein is modulated. The compositions, proteins, polynucleotides and methods are useful for treating and detecting cancer. The STEAP-1-related proteins are useful for generating cancer vaccines. The polynucleotides are useful as tools for delineating, with greater precision, cytogenetic abnormalities in the chromosomal region that encodes STEAP-1 that may contribute to the malignant phenotype. This is the amino acid sequence of a variant of human six transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modulates the status of a protein (I) of 340 or 283 amino acids, or of any of the 15 sequences of 259 amino acids, given in the specification, or a molecule that is modulated by the protein, where the status of the cell that expresses the protein is modulated. The compositions, proteins, polynucleotides and methods are useful for treating and detecting cancer. The STEAD-1-related proteins are useful for generating cancer vaccines. The polynucleotides are useful as tools for delineating, with greater precision, cytogenetic abnormalities in the chromosomal region that encodes STEAP-1 that may contribute to the malignant phenotype. This is the amino acid sequence of a variant of human six transmembrane epithelial antigen of the prostate or STEAP-1
epithelial antigen
                                                                                                                                                                                                                                                                                                                                                        Example
                                                                                                                                                                                                                                                                                                                                                                                                              STEAP-1-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-313240/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-SEP-2001; 2001US-0317840P
05-APR-2002; 2002US-0370387P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STEAP-1; six transmembrane epithelial antigen of the prostate; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Faris M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-SEP-2002; 2002WO-US028371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STEAP-1 variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU98424 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AGEN-) AGENSYS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003022995-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REVIHELATSHOOYFYKIPILV 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ge W,
                                                                                                                                                                                                                                                                                                                                                  Page 169; 248pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                        comprising a substance that modulates the status of a protein, useful for treating and detecting cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                delineation; cytogenetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8P1D4 v.2 #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Raitano
of the
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prostate or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 116; DB 6
Pred. No. 2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                  for treating and detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
STEAP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   abnormality; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                     cancer.
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RESULT 15 ABU98387

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ABU98392
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                                                 Query Match
Best Local S
Matches 22
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                                                                                                                     The invention describes a composition comprising a substance that modulates the status of a protein [1] of 340 or 283 amino acids, or of any of the 15 sequences of 259 amino acids, given in the specification, or a molecule that is modulated by the protein, where the status of the cell that expresses the protein is modulated. The compositions, proteins, polynucleotides and methods are useful for treating and detecting cancer. The STEAP-1-related proteins are useful for generating cancer vaccines. The polynucleotides are useful as tools for delineating, with greater precision, cytogenetic abnormalities in the chromosomal region that encodes STEAP-1 that may contribute to the malignant phenotype. This is the amino acid sequence of a variant of human six transmembrane epithelial antigen of the prostate or STEAP-1
                                                                                                   Sequence 258
                                                                                                                                                                                                                                                                                                  Example
                                                                                                                                                                                                                                                                                                                     New composition comprising a substance that modulates the status of a STEAP-1-related protein, useful for treating and detecting cancer.
                                                                                                                                                                                                                                                                                                                                                                                                      Faris M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-SEP-2001;
05-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAR-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU98392 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                              (AGEN-) AGENSYS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human gene STEAP-1 variant 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JUL-2003
                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                              2; Fig 2J; 248pp; English.
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REVIHELATSHOOVEYKIPILV 113
                         REVIHPLATSHQQYFYKIPILV
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                                                 Conservative
                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; ilarity 100.0%; Conservative
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2002US-0370387P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               delineation;
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                                                            100.0%;
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cytogenetic abnormality; cytostatic;
                                                            Score 116; DB 6
Pred. No. 2e-10;
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Pred. No. 2e-10;
Mismatches
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                                                 Mismatches
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Search completed: July 12, 2004, 14:07:22 Job time: 48.3488 secs
                                                                                                                                                                                                                                                 Query Match 100.0%; Score 116; DB 6; Best Local Similarity 100.0%; Pred. No. 2e-10; Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                The invention describes a composition comprising a substance that modulates the status of a protein (I) of 340 or 283 amino acids, or of any of the 15 sequences of 259 amino acids, given in the specification, or a molecule that is modulated by the protein, where the status of the cell that expresses the protein is modulated. The compositions, proteins, polynucleotides and methods are useful for treating and detecting cancer. The STERAP-1-related proteins are useful for generating cancer vaccines. The polynucleotides are useful as tools for delineating, with greater precision, cytogenetic abnormalities in the chromosomal region that encodes STERAP-1 that may contribute to the malignant phenotype. This is the amino acid sequence of a variant of human six transmembrane epithelial antigen of the prostate or STEAP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-SEP-2001; 2001US-0317840P.
05-APR-2002; 2002US-0370387P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human gene STEAP-1 variant 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003022995-A2
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence 258 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Fig 2E; 248pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New composition comprising a substance that modulates the status of a STEAP-1-related protein, useful for treating and detecting cancer.
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                                                                                                                                                                                                                                                           Score
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    protein search, using sw model
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1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*
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93
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sp_phage:*
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sp_virus:*
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sp_mhc:*
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1 Q924J9
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1 Q9CWR7
1 Q9CWR7
6 Q8F0P8
6 Q98CK3
5 Q8JF92
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Q986k3 rhizobium l
Q8jf92 human immun
Q8uht8 agrobacteri
Q9jj19 human immun
Q90702 human immun
Q90702 human immun
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Q97002 human immun
Q9evq0 escherichia
Q8haj1 bacteriopha
Q90dn6 human immun
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089292 human		Q8q2x4 human		Q9qkh9 human	Q9qki4 human	Q8q2x3 human	Q7svk2 human	Q7svk3 human	Q7svk4 human		Q8buh3 mus	Q78120 human	Q8au20 human	Q8jeq9 human	Q8jer0 human	Q8jer2 human	Q90e72 human	Q8jer1 human	Q8j3q3 human	Q7sm42 human	Q7sm24 human	Q8ura0 human	Q8uqy9 human	Q8uqz0 humar	Q7zjr5 humar	Q7zjr8 humar	Q9qiu8 human	Q9ill6 human
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ALIGNMENTS

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RESULT
Q924J9
ID Q9
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Matches 13
Q924J9
Q924J9;
01-DEC-2001
01-DEC-2001
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Six transmembrane endothelial antigen of PAEC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                  Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF319659; AAG33868.1; -. GO; GO:0016021; C:integral to membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                    Nagasaka T., Boulday G., Coupel S., Coulon F., Tesson L., Heslan J.-M., Soulillou J.-P., Charreau B.; "Differential gene expression in endothelial cells during and LPS-mediated activation.";
                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                      Transmembrane.
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                                                                                                                                                                 1 WIDIKQEVWYTPPTF 15
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WVDIKQFIWYTPPTF 290
                                                                                                                                                                                                                                                                     338 AA;
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                                                  PRELIMINARY;
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                                                                                                                                                                                                  97.8%; Score 91; DB 86.7%; Pred. No. 1.1e tive 2; Mismatches
Last sequence update
                 Created)
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RESULT 3
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DT 01-C
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DE DUdu
GN STEAR
OS Mus
OC Euka
OC Mamm
OX NCB1]
RN (1)
RN (1)
RP SEQ1
RA Serz;
RESULT 4
Q9CWR7
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01-JUN-2001 |
01-JUN-2001 |
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Q924Z2;
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                                                                                                                                                                                       Q9CWR7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Prostate and non-prostate expression of of human STEAP."; Submitted (APR-2001) to the EMBL/GenBank/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
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   2410007B19Rik protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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Serru V., Manivet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STEAP
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A; 39109 MW;
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Pred. No. 6.6e
2; Mismatches
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brane antigen: prostate-
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Hordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
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                                                                                                                 EMBL; AE011502; AAN50642.1; -...
InterPro; IPR001466; Beta lactamase.
InterPro; IPR000437; ProK lipoprot_S.
Pfam; PF00144; beta-lactamase; 1.
PROSITE; PS00013; PROKAR LIPOPROTEIN;
Hypothetical protein; Complete proteom
SEQUENCE 419 AA; 47652 MW; BE6FE7C
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EMBL; AK010437; BAB26938.1;
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STRAIN-C57BL/6J; TISSUE-Embryonic stem cells;
MEDLINE-21085660; PubMed-11217851;
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                Similarity 7; Conserv
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BE6FE7CF180F0B80 CRC64;
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                                                               Jones D.R., Suzuki K., Filler S.C.;

"A 100-Amino Acid Truncation in the Cytoplasmic Tai
41 in the Reference HIV Type 1 Strain RF ";
AIDS Res. Hum. Retroviruses 18:513-517(2002).
EMBL; AF403705; AAM21476.1; -
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEJ
InterPro; IFR00328; Env GP41.
Pfam; PF00517; GP41; 1.
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01-OCT-2001
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01-OCT-2002 (TrEMBLrel. 22, Last seque)
01-UN-2003 (TrEMBLrel. 24, Last annot
Truncated envelope protein (Fragment).
Human immunodeficiency virus 1.
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Q8JF92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0005215; F:transporter activity; GO; GO:0006810; P:transport; IEA.
InterPro; IER006059; SBP_bac_1.
Pfam; PF01547; SBP_bac_1; 1.
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                                               Envelope
                                                                                                                                                                                                                                                                                              MEDLINE=22011541; PubMed=12015905;
                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
... ren transporter, substrate-binding
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                                               Transmembrane.
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Pred. No.
2; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation updat
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4F0058F96DE1C48B CRC64;
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A., Kawashima K., Kimura
I., Matsumoto M., Matsuno
ki N., Shimpo S., Sugimot
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                                                                                                                                                                                                                                             Tail of Glycoprotein
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imura T.,
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Matches 7
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Best Local
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PIR; AB2649; AB2649.

GO; GO:0005215; F:transport; IEA.

GO; GO:0006810; P:transport; IEA.

InterPro; IPR006059; SBP_bac_1.

Pfam; PF01547; SBP_bac_1; 1.
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Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Gran
Rutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.
Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P.,
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W.,
Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Clson M.
                                                                                                                                                                                                                                                    Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.;
                                                                                                                                                                                            Agrobacterium tumefaciens C58. 
Science 294:323-2338 (2001). 
EMBL; AE009027; AA141608 1; -.
                                                                                                                                                                                                                                                                                                                                                         C58.";
Science 294:2317-2323(2001).
[2]
                                                                                                                                                                                                                                                                                                                                                                                           Nester
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Agrobacterium tumefaciens (strain)
                                                                                              SEQUENCE
                                                                                                          Complete
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01-JUN-2002
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                                                                                                                                                                                                                                                                                                                              MEDLINE=21608551; PubMed=11743194;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Proteobacteria; Alphaproteobacteria; RhizoRhizobiaceae, Rhizobium/Agrobacterium group; Agroba
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                                                                                                                                                                                                                                 "Genome sequence of the plant pathogen and Agrobacterium tumefaciens C58.";
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                                                                                                                                                                                                                                                                                                                                                                                           genome
169
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                                              Similarity 7; Conserv
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                     DIKOFVWYTPPTF
                                                                                                        proteome.
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                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                           natural genetic
                                                                                             49090 MW;
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                                                        51.6%;
181
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Last annotation updat
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                                                        Score 48; DB
Pred. No. 15;
                                                                                                                                               IEA.
                                                                                                                                                         activity;
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                                                                                            90896249313CD85E
                                              Mismatches
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                                                                      16;
                                                                                                                                                                                                                                           biotechnology agent
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                                                                     Length 453;
                                                                                             CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grant C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sr.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Perry
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RESULT Q9IJL9

Q9IJL9

PRELIMINARY;

122

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RESULT 10
Q97002
ID Q9700
AC Q9700
AC Q9700
AC Q9700
DT 01-FB
DT 01-JU
DT ENVel
GN ENV.
OS HUMAN
OC NCEI
GN ENV.
OS NCEI
GN EN CI
GN EN CO
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Best Local
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01-OCT-2000
01-OCT-2000
01-JUN-2003
EMBL; U27401; AAB06242.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
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"Evidence for a high frequency of HIV-1 subtype F infections among heterosexual population in Buenos Aries, Argentina.";
AIDS Res. Hum. Retroviruses 16:1007-1014 (2000).
EMBL, AF220713; AAF76632.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0015198; F:structural molecule activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1997 (TrEMBLrel. 02,
01-FEB-1997 (TrEMBLrel. 02,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96190564; PubMed=8627686;
Gao F., Morrison S.G., Robertson D.L.,
Karlsson G., Sodroski J., Morgado M., (
von Briesen H., Beddows S., Weber J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus 1. Viruses; Retroid viruses; Retro NCBI_TaxID=11676;
                                                                                                                                                                                 Allen E.E.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                      STRAIN=HIVBR020.17;
                                                                                                                                                                                                                                                                                                                                                                                            WHO and NIAID Networks for HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hahn B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=HIVBR020.17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Envelope
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01-FEB-1997
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Viruses; Retroid viruses; Retroviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Envelope glycoprotein (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Molecular cloning and analysis of functional
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                                                                                                                                                                                                                                                                                                                                                        Virol.
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122 AA;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46; DB Pred. No. 8.3; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                         sis of functional envelope genes from type 1 sequence subtypes A through G. IV Isolation and Characterization.";
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01-MAR-2001
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InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
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"Structural analysis of phage-borne stx genes and sequences in shiga toxin-producing escherichia col dysenteriae type 1 strains.";
Infect. Immun. 68:4856-4864(2000).
EMBL; AJ251452; CACO5542.1; -
Hypothetical protein.
SEQUENCE 107 AA; 12177 MW; 8BCD6C52B7D29CE6 CF
                                                    Muniesa M., Jofre J.;
"Variability of shiga converting
strains of human origin isolated
submitted (SEP-2002) to the EMBL,
EMBL, AF548456; AAN59922.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein. Escherichia coli.
   Hypothetical SEQUENCE 1
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STRAIN=159;
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107 AA; 1:
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Pred. No. 11;
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      8BCD6C52B7D29CE6 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last:
01-JUN-2003 (TrEMBLrel. 24, Last:
Envelope glycoprotein (Fragment).
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SEQUENCE
"Genotyping and phenotyping analysis of immunodeficiency virus type 1 subtypes f Submitted (UUL-1999) to the EMBL/GenBank EMBL, AF16537, AAF08482.1; -. GO; GO:0016021; C:integral to membrane; GO; GO:0019031; C:viral envelope; IEA.
                                                                                                                          Caride E., Hertogs K., Larder E
Machado E., de Sa C.A.M., Eyer
Calazans A.R., Tanuri A.;
                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=GP41ERRJ04;
                                                                                                                                                                                                                                                                          Human immunodeficiency virus 1. Viruses; Retroid viruses; Retro
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ
EMBL; AF307695; AAL08756.1;
G0; G0:0016021; C:integral to membrane; IEA.
G0; G0:0019031; C:viral envelope; IEA.
G0; G0:0005198; F:structural molecule activity
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                         NCBI_TaxID=11676;
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SUMMARIES

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Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
Pohl T., Portetelle D., Puehler A., Weidner S., Galibert F.;
"Analysis of the chromosome sequence of the legume symbiont
Sinorhizobium mellioti strain 1021";
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
-i- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
FOR ALEPHA-GLUCOSIDES SUCH AS SUCROSE, MALTOSE AND TREHALOSE.
-i- SUBCELLULAR LOCATION: Periplasmic (Probable).
-i- SIMILARITY: Belongs to the bacterial extracellular solute-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alpha-glucosides-binding periplasmic protein aglE precursor
AGLE OR R00695 OR SWC03061.
Rhizobium meliloti (Sinorhizobium meliloti).
Rhizobium meliloti (Sinorhizobium meliloti).
Rhizobian proteobacteria, Alphaproteobacteria, Rhizobiales;
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EMBL; AC005053; AAC79150.1;
EMBL; AC004969; AAD15620.2;
EMBL; BC011802; AAH11802.1;
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MEDLINE=99328961; PubMed=10400573;
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30-MAY-2000
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GO; GO:0005911; C:intercellular junction; TAS.
GO; GO:0015267; F:channel/pore class transporter ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                               MEDLINE=21396507; PubMed=11481430;
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                          "A novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGLE RHIME
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                                             protein family 1.
SWISS-PROT entry is copyright. It is produced through a deep the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                       TaxID=382;
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                                                                                                                                                                                                                                                                                                                                        vel Sinorhizobium meliloti operon encodes an alpha-glucosidase
periplasmic_binding-protein-dependent transport system for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HGNC:11378; STEAP
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llarity 100.0%;
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Pred. No. 7.4
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              a collaboration
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EMBL; AL591784; CAC45267.1; -.
InterPro; IPR006059; SBP_bac_1.
InterPro; IPR006061; SBP_domI.
Pfam; PF01547; SBP_bac_1; 1.
PROSITE; PS01037; SBP_BACTERIAL_1; FALSE_NEG.
SUGUAT transport; Transport; Periplasmic; Signal; Complete
SIGNAL_1
27
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=86218077; PubMed=2423250; McNeely P.D., Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., I "Identification and characterization of conserved regions in the envelope gene of HTLV-III/LAV, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-AUG-1987 (Rel. 05, Last sequence update)
15-UL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein GP160 precursor [Contains:
glycoprotein (GP120); Transmembrane glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                    InterPro; IPR000328; Env_GP41.
InterPro; IPR000777; GP120.
Pfam; PF005516; GP120; 1.
Pfam; PF00517; GP41; 1.
                                                                                                                                                                                                                                                                                                                    EMBL; M17451; AAA45057.1; -. HIV; M17451; ENV$RF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regions in the envelope gene AIDS.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus type 1 (RF/HAT isolate) Viruses; Retroid viruses; Retroviridae; Lentivirus. NCBI_TaxID=11701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-AUG-1987 (Rel. 05,
13-AUG-1987 (Rel. 05,
15-UUL-1999 (Rel. 38,
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13-AUG-1987
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EXTERIOR MEMBRANE GLYCOPROTEIN.
TRANSMEMBRANE GLYCOPROTEIN.
BY SIMILARITY.
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Pred. No.
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Q01371;
01-NOV-1997
16-OCT-2001
16-OCT-2001
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                                                                                                                                STRAIN-74-OR23-1A / FGSC 987;
MEDLINE-96203083; PubMed-8612589;
Ballario P., Vittorioso P., Magre
                                                                                                                                                                                                                                                      Neurospora crassa.
Eukaryota; Fungi; Ascomycota;
Sordariomycetidae; Sordariales
NCBI_TaxID=5141;
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                        White collar WC-1.
                                       "White collar-1, a central regulator Neurospora, is a zinc finger protein. EMBO J. 15:1650-1657(1996).
                                                                                                                 Macino G.
REVISIONS
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
1 protein (WC1).
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N-LINKED (GL
                                                                                                                                       Magrelli
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s; Sordariaceae;
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(GECNA
                                                                                        blue light responses
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                                                                                                                                       Talora C.,
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                                                                                                                                                                                                                                                                                 Sordariomycetes;
Neurospora.
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RESULT 5
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AC Q87AI9;
DT 10-OCT-2003 1
DT 10-OCT-2003 1
DT 10-OCT-2003 1
DE Organic solve
GN IMP OR OSTA 0
OS Xylella fast;
OC Bacteria; Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            $\frac{1}{2} \frac{1}{2} \frac
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSFAC; T02819; -. PAC.
InterPro; IPR001610; PAC.
InterPro; IPR000014; PAS domain.
InterPro; IPR000679; Znf GATA.
Pfam; PF00785; PAC; 1.
Pfam; PF00785; PAC; 1.
Pfam; PF00989; PAS; 2.
SMART; SM000916; PAC; 2.
SMART; SM00091; PAS; 3.
SMART; SM00091; ZnF GATA; 1.
TIGREAMS; TIGR00229; Sensov; Dox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nuclear protein; F
DOMAIN 381
DOMAIN 469
DOMAIN 574
DOMAIN 650
DOMAIN 693
ZN FING 934
DOMAIN 21
DOMAIN 21
DOMAIN 329
SEQUENCE 1167 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY FUNCTION AS A TRANSCRIPTION FACTOR INVOLVED IN LIGHT REGULATION OF THE AL-3
GENE. WC1 AND WC2 PROTEINS INTERACT VIA HOMOLOGOUS PAS DOMAINS,
BIND TO PROMOTERS OF LIGHT REGULATED GENES SUCH AS FRQ, AND
                  10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Organic solvent tolerance protein precursor.
IMP OR OSTA OR PD1836.
Xylella fastidiosa (strain Temeculal / ATCC 700964).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ballario
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or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene expression.
SIMILARITY: Contains 1 GATA-type zinc fing
SIMILARITY: Contains 3 PAS (PER-ARNT-SIM)
SIMILARITY: Contains 2 PAS-associated C-ty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTIVATE TRANSCRIPTION.
SUBUNIT: HETERODIMER OF WC1 AND
SUBCELLULAR LOCATION: Nuclear.
INDUCTION: By blue light.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN: The glutamine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X94300;
P17679;
                                                                                                                                                                                                                                                                                             529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ms; TIGR00229; sensory box; 3.
3; PS00344; GATA ZN FINGER 1; 1
3; PS50114; GATA ZN_FINGER_2; 1.
3; PS50112; PAS; 3.
4 iption recovery.
                                                                                                                                                                                                                                                                                                                                       W
                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          non-profit institutions as long and this statement is not removed. requires a license agreement (See an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                           DIGQYIW-TPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₽.;
                                                                                                                                                                                                                                                                                                                                       DIKQFVWYTPPT
    Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1GNF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAA63964.2; -.
                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ĀΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repeat.
452
508
644
691
763
959
                                                                                                                                                                                                                                                                                                                                                                                                      46.8%;
66.7%;
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                                                                                                                                                                                                                                                                                             539
                                                                                                                                                                                                                                                                                                                                       14
  Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Activator; DNA-binding; Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAS (PER-ARNT-SIM) dimerization PAS-associated C-terminal (PAC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MW;
                                                                                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLN-RICH.
PAS 1.
PAS 1.
PAC 2.
PAC 2.
PAC 2.
PAC 3.
GATA-TYPE.
POLY-GLN.
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                          Score 43.5;
Pred. No. 3
                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6489D04DAB50EE38 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WC2
                                                                                                                                                                                792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 might
                                                                                                                                                                                                                                                                                                                                                                                                          32;
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                                                                                                                                                                                                                                                                                                                                                                                                                             1;
    Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1167;
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Xanthomonadaceae; Xylella

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OPSP
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                            042266;
042266;
15-JUL-1998 (Rel. 3
15-JUL-1998 (Rel. 3
10-OCT-2003 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B., Miyaki C.Y., Furlan I.R., Camargo L.E.A., da Silva A.C.R., Moon D.H., Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R., Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorry H., Tsai S.M., Carrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J., Coutinho L.L., Kimura E.T., Ferro E.S., Harakava R., Kuramae E.E., Marino C.L., Giglioti E., Abreu I.L., Alves L.M.C., do Amaral A.M., Marino C.L., Giglioti E., Abreu I.L., Alves L.M.C., do Amaral A.M., Marino G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V., da Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T., Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sassaki F.T., Sena J.A.D., de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zaros L.G., Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        _dssp_
_uspu_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF04453; OstA C; 1.

Pfam; PF04453; OstA C; 1.

Outer membrane; Signal; Complete proteome.

POTENTIAL.

22

POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                           MEDLINE=97477428; PubMed=9334384; Blackshaw S., Snyder S.H.;
                                                                                                                                                                             Ictalurus punctatus (Channel catfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriforme
Ictaluridae; Ictalurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAMAP; MF_01411; -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Comparative analyses of the complete genome sequences of Pierce's disease and citrus variegated chlorosis strains of Xylella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kitajima J.P.;
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[1]
   "Parapinopsin,
                                                                                         SEQUENCE FROM N.A.
                                                                                                                                              NCBI_TaxID=7998
                                                                                                                                                                                                                                                                                                      Parapinopsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE012560; AA029668.1; -.
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Van Sluys M.A., d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteriol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Belongs to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Determines N-hexane tolerance. Involved in outer membrane permeability. Essential for envelope biogenesis. Could be part of a targeting/usher system for outer membrane components (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Outer membrane (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ICTPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       440
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR007543; OSTA_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      792 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23
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a novel catfish opsin localized to the parapineal
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; PubMed=12533478; de Oliveira M.C.,
                                                                                                                                                                                                                                                                                                                            36,
42,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.2%;
                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                          Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANIC SOLVENT TOLERANCE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                            Siluriformes;
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RESULT
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Best Local
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BINDING
                                         p46992;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence updat
01-OCT-1996 (Rel. 34, Last annotation upon
Hypothetical 43.0 kDa protein in CPS1-FP)
YJL171C OR J0512.
                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPRO00276; GPCR_Rhodpsn.
InterPro; IPR001760; Opsin.
Pfam; PP00001; 7tm 1; 1.
PRINTS; PR00237; GFCRRHODDSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00238; GPROTEIN_RECEP_F1_2; 1.
PROSITE; PS00238; OPSIN; 1.
Photoreceptor; Retinal protein; Transmembr;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a cetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organ, defines a new gene family.";
J. Neurosci. 17:8083-8092(1997).
-i- SUBCELIJULAR LOCATION: Integral membrane protein.
-i- TISSUE SPECIFICITY: PARAPINEAL ORGAN.
-i- PIM: Some or all of the carboxyl-terminal Ser or Thr residues may be phosphorylated (By similarity).
-i- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                    Saccharomycetales;
                                                                                                                                          YEAST
                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF028014; AAB84050.1; -. HSSP; P02699; 1FDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                               Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phosphorylation;
DOMAIN 1
                                                                                                                               YJR1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Opsin subfamily.
                                                                                                                              YEAST
                                                                                                                                                                                      158 FIWNTPPLF 166
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                                                                                                                                                                                                                                    6;
                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                             FVWYTPPTF 15
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315
346 ]
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170
                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                 AA;
                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lipoprotein;
                      Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                      191
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169
193
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66
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106
126
                                                                                                                                                                                                                                              45.2%;
66.7%;
                                                                                                                                                                                                                                                                                 38203 MW;
                                                                  Last annotation update) protein in CPS1-FPP1 intergenic region.
                                                                              Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                               N-LINKED (GLONAC. ...) (POTENTIAL).
N-LINKED (GLONAC. ...) (POTENTIAL).
S-palmitoyl cysteine (By similarity);
A70871684F8FC7FD CRC64;
                                                                                                                                                                                                                                               Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                             RETINAL CHROMOPHORE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC
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                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR
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                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Transmembrane; Glycoprotein; Palmitate; G-protein coupled r
                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
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                                                                                                                                                                                                                                     Mismatches
                                                                                                                              396
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                                                                                                                              A
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                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
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                                                                                                                                                                                                                                                        Length 346;
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RESULT ERF 2-YE IN FRANCE OF STANFORM OF S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P05453; P05420;
P05453; P05420;
01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Eukaryotic peptide chain release factor GTP-binding subunit (ERF2)
(Translation release factor 3) (ERF3) (CRF-3) (Omnipotent suppress protein 2) (G1 to S phase transition protein 1).

Protein 2) (G1 to S phase transition protein 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YEAST
ERF2_1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Saccharomycetales; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGD;
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                            SEQUENCE FROM N.A.
MEDLINE=88296422; PubMed=2841115;
Kukuchi Y., Shimatake H., Kikuchi
                                                                                                                                                    J. Mol.
                                                                                                                                                                                                                                               Wilson P.G., Culbertson
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=88172503; PubMed=3280807;
                                                                                                                                                                                                                                                                                                                                                                       FEBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=87219095; PubMed=3556215; Kushnirov V.V., Ter-Avanesyan M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kushnirov V.V., Ter-Avanesyan M.D., Smirnov V.N., Inge-Vechtomov S.G.; "Nucleotide sequence of the SUP2 (S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      Inge-Vechtomov S.G.;
"Localization of possible functional domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4932;
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                                                                                                                                                 on P.G., Culbertson M.R.;
12 suppressor protein of yeast.;
family of elongation factors.";
ol. Biol. 199:559-573(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66:45-54 (1988).
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                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cere . 215:257-260(1987)
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396 AA; 4
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required
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chi A.;
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Best Local S
Matches 7
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InterPro; IPR004160; BFTU Cterm.
InterPro; IPR004161; BFTU D2:
InterPro; IPR009001; Elong init C.
InterPro; IPR009000; Translat factor.
Pfam; PF00104; GTP EFTU; 1.
Pfam; PF00144; GTP EFTU D2; 1.
Pfam; PF03143; GTP EFTU D3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M21129; AAA3513;
EMBL; X07163; CAA30155
EMBL; Y00829; CAA6876;
EMBL; Z46727; CAA86677
PIR; S00733; EFBYS2.
GermOnline; 140663; --
                                                                                                                                                                                MOD_RES
CONFLICT
                                                                                                                                                                                                                       NP_BIND
NP_BIND
NP_BIND
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; I PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation termination in Saccharomyces cerevisiae EMBO J. 14:4365-4373(1995).
-!- FUNCTION: INVOLVED IN TRANSLATION TERMINATION.
                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stansfield I., Jones K.M., Kushnirov V.V., Dagkesamanskaya A.R., Poznyakovski A.I., Paushkin S.V., Nierras C.R., Cox B.S., Ter-Avanesyan M.D., Tuite M.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           containing an A-kinase ta
EMBO J. 7:1175-1182(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTIVITY OF ERF1. BINDS GUANINE NUCLEOTIDES.
SUBUNIT: Heterodimer of two subunits, one of which binds GTP.
SUBCELLULAR LOCATION: Cytoplasmic (Probable).
SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S0002579; SUP35.
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                                                                            7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                      PR00315; ELONGATNECT.; PS00301; EFACTOR_GTP;
                                                                                                                                                                                                                                                                                                                                                                     biosynthesis;
VDPKECPWYTGPT
                                    IDIKQFVWYTPPT
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., Harris D.E., 1
1 (NOV-1994) to
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685
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                                                                              Conservative
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; CAA68760.1;
; CAA86677.1;
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GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

INTERACT WITH GTP/GDP (BY SIMILARITY).

INTERACT WITH GTP/GDP (BY SIMILARITY).

PHOSPHORYLATION (BY SIMILARITY).

S -> C (IN REF. 4).
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CHARGED.
GTP (BY SGTP (BY SGTP
                                                                                                                     Score
                                                                                                  Pred.
                                                                                                                                                                                                                                                                                                                                              Phosphorylation;
SEVERAL SORT OF RE
                                                                                                                                                             43912A6D77DFA153
                                                                                Mismatches
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No.
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(See http://www.isb-sib.ch/announce/
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32;
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MBL; AF316985;
HSSP; O60603; 1FYW.
HSSP; O60603; 1FYW.
MGD; MGI:1341295; Tlr1.
GG; GG:0016020; C:membrane; NAS.
GG; GG:0016020; C:phagocyric vesicle; NAS.
GG; GG:00045335; C:phagocyric vesicle; NAS.
GG; GG:00045335; C:phagocyric vesicle; NAS.
GG; GG:0004497; F:triacylated lipoprotein binding; NAS.
GG; GG:00042497; F:triacylated lipoprotein binducing kinase; NAS.
GG; GG:00042497; P:activation of NF-kappaB-inducing kinase; NAS.
GG; GG:00042497; P:perception of triacylated bacterial lipopro.
R GG; GG:0042495; P:perception of triacylated bacterial lipopro.
DR GG; GG:0042495; P:perception of triacylated bacterial lipopro.
GG; GG:0042495; P:perception of triacylated bacterial lipopro.
TPR004075; ILL receptor1.
TPR004075; ILL receptor1.
TPR001611; LRR.
TPR Cterm.
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Thomson D.P., Campbell C.C., Liew F.Y., Xu D.;
Thomson D.P., Campbell C.C., Liew F.Y., Xu D.;
"Cloning of Mus musculus Toll-like receptor 1.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: Participates in the innate immune response to microbial agents. Cooperates with TLR2 and modulates the response to microbial constituents. Acts via MyD88 and TRAF6, leading to NF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AY009154; AAG37302.1;
EMBL; AF316985; AAG35062.1;
HSSP; 060603; 1FYW.
MGD; MGI:1341295; Tlr1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Functional interactions between Toll-like receptor (TLR) 2 and TLR1 or TLR6 in response to phenol-soluble modulin.";
J. Immunol. 166:15-19(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Macrophage;
MEDLINE=20571875; PubMed=11123271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ozinsky A., Underhill D.M., Fontenot J.D Wilson C.B., Schroeder L., Aderem A.; "The repertoire for pattern recognition immune system is defined by cooperation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BALB/c; TISSUE=Macrophage; MEDLINE=20558581; PubMed=11095740;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 'Toll-like receptor (TIL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This
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28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in ified and this statement is not removed. Usage by and for compared the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phagosomes.
SIMILARITY: Belongs to the Toll-like receptor family.
SIMILARITY: Contains 1 TIR domain.
SIMILARITY: Contains 9 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                kappa-B activation, cytokine secretion and the inflammatory response (By similarity). SUBUNIT: Binds TLR2 via their respective extracellular domains. Binds MyD88 via their respective TIR domains (By similarity). SUBCELLULAR LOCATION: Type I membrane protein. Plasma membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            requires a
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41, Last sequence update)
41, Last annotation update)
41, Iast annotation update)
7 1 precursor (Toll/interleukin-1 receptor-like)
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Rodentia;
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Best Local
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P19550;
01-FEB-1991
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This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo
                                                                                                                                                                                                                                                                                          01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Envelope polyprotein GP100 precursor (Contains:
glycoprotein (GP120); Transmembrane glycoproteir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
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DOMAIN
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Pfam; PF01582; TIR; 1.
PRINTS; PR01527
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REPEAT
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SMART; SM00255; TIR; 1.
                                                                                                                                      MEDLINE=90347835;
Cheng-Mayer C., Qu
"Viral determinant
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                                                                                                                     macrophage
                                                                                                                                                                                                                                          Viruses;
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                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                        NCBI_TaxID=11691;
                                                                                                                                                                                                                                          Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264
                                                                                                                  Mayer C., Quiroga M., Tung J.W., Dina D., Levy J.,
determinants of human immunodeficiency virus type 1
hage tropism, cytopathogenicity, and CD4 antigen mod
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                                                                                                     e tropism, cytopatho 64:4390-4398(1990).
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                Eukaryota; Fungi; F
Saccharomycetales;
                                                        Saccharomyces cerevisiae (Baker's yeast).
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M38428; ENV$SF162.
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Coat protein; I
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IPR000777; GP120.
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a
                                     Ascomycota;
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50.0%;
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protein in TIM23-ARE2 i
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                              Saccharomycotina; Saccharomycetes,
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              Saccharomyces
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01-NOV-1997 (Rel. 35, 0
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                                                                                                                                                                                                                            STRAIN=K12;
Reeves P.R.;
Submitted (1
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Pfam; Pr04588; HIG 1 N; 1.
Hypothetical protein; Transmemb
TRANSMEM 19 39 PC
TRANSMEM 50 70 PC
TRANSMEM 152 172 PC
DOMAIN 196 199 PC
      Science
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ECOLI
WCAD
                                                         STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blatther F.R., Plunkett G. III, Bloch
Riley M., Collado-Vides J., Glasner J.
Gregor J., Davis N.W., Kirkpatrick H.A
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                         J. Bacteri
[2]
REVISIONS
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DOMAIN
"The complete genome sequence
Science 277:1453-1474(1997)
-!- PATHWAY: Slime polysacchar
                                                                                                                                                                                                                                                                                                                           MEDLINE=96326333; PubMed=8759852;
Stevenson G., Andrianopoulos K., Hobbs M., Reeves P.R.;
Stevenson of the Escherichia coli K-12 gene cluster responsible
"Organization of the Escherichia coli K-12 gene cluster responsible
for production of the extracellular polysaccharide colanic acid.";
10. Bacteriol. 178:4885-4893(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterobacteriaceae;
NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia
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STRAIN=K12
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the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through
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TRANSMEM
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GermOnline; 143363; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pohl T.M.; Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
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57.1%;
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Pred. No. 12;
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RESULT 13
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RX MEDLINE=98044033; PubMed=9384377;
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., BrA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., BrA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., BrA Azevedo V., Bertero M.G., Braun M., Brignell S.C., Bron S., RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., RA Borriss R., Codani J.J., Connerton I.F., Cummaings N.J., Daniel R.A., RA Choi S.K., Codani J.J., Connerton I.F., Cummaings N.J., Daniel R.A., RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., RA Fritz C., Fujita M., Fujita Y., Fabret C., Ferrari E., Foulger D., Farrington J., Fabret C., Ferrari E., Foulger D., Valler M., Forliger D., Farrington J., Fabret C., Ferrari E., Foulger D., Farrington J., Fabret C., Forandi G., Gulghtly E.J., Grandi G., Ra Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Ra Kurita K., Lapidus A., Lardinois S., Laber J., Lazarevic V., RA Kurita K., Lapidus A., Lardinois S., Laber J., Lazarevic V., RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C., RA Rieger M., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., Parro V., Pohl T.M., Schleich S., Schroeter R., Scoffone F., RA Rieger M., Rivolta C., Rocha E., Roche E., Rose M., Sadaie Y., RA Rieger M., Schwska A., Seror S.J., Serror P., Shin B.S., Soldo B., Rapotin J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Rapotin K., Wata K., Yata 
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15-JUL-1998 (Rel. 3
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PUCK_BACSU
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                    "The complete genome sequence subtilis.";
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   Nature 390:249-256(1997).
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CONFLICT 108 108 P -> A (IN REF. 2).
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42, Last annotation
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45409 MW; A3D9D91255686043 CRC64;
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"Functional analysis of 14 genes that constitute the purine catabolic pathway in Bacillus subtilis and evidence for a novel regulon controlled by the Puck transcription activator.";

J. Bacteriol. 183:3293-3302(2001).

-I- FUNCTION: Uptake of uric acid.

-i- SUBCELIULAR LOCATION: Integral membrane protein (Probable).

-i- SUBCELIULAR induced during limiting-nitrogen conditions (glutamate plus ammonia) and is induced during limiting-nitrogen conditions (glutamate). Expression is further induced when allantoin or uric acid are added during limiting-nitrogen conditions.

-i- SIMILARITY: BELONGS TO THE XANTHINE/URACIL PERMEASES FAMILY.
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TRANSMEM
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modified and this statement is not removed.
entities requires a license agreement (See l
or send an email to license@isb-sib.ch).
                        Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomycetaceae;
                                                                                                              Q8TFF6;
10-OCT-2003
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InterPro; IPR006042; Xan ur permease.
InterPro; IPR006043; Xant/urac/vitC.
Pfam; PF00860; xan_ur_permease; 1.
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PROSITE; PS01116; XA
            NCBI_TaxID=4931;
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the European Bioinformatics Institute.

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SIMILARITY: TO ARYB, TARTHROPOD HEMOCYANINS.

TO B.MORI

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NP BIND
SEQUENCE
                                                                               hemocyanins.";

J. Biol. Chem. 264:19052-19059(1989).

J. Biol. Chem. 264:19052-19059(1989).

J. FUNCTION: Arylphorin is a larval storage protein (LSP) which may serve as a storage protein used primarily as a source of aromatic amino acids for protein synthesis during metamorphosis. It is a constituent of the sclerotizing system of the cuticle, and serves as a carrier for ecdysteroid hormone.
                                                                                                                                                                                                                                                                                         MEDLINE=90037032; PubMed=2808410; Willott E., Wang X.-Y., Wells M.A.; Willott E., Wang X.-Y., Wells M.A.; "cDNA and gene sequence of Manduca sexta arylphorin, an axomatic amino acid-rich larval serum protein. Homology to arthropod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New S. pastorianus strains and Saccharomyces natural hybrids revealed by polyphasis identification of CBS strains formerly uncompletely identified by conventional method.";

Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: L-glutamate + H(2)O + NADP(+) = 2-oxoglutarate + NH(3) + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=Larval fat body;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=7130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oxidoreductase; NADP.
ACT_SITE 110 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00208; GLFV_dehydrog; 1.

Pfam; PF02812; GLFV_dehydrog_N; 1.

PRINTS; PR00082; GLFDHDRGNASE.

PROSITS; PS00074; GLFV_DEHYDROGENASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR006095; GLFV dehydrog C. InterPro; IPR006096; GLFV dehydrog C. InterPro; IPR006097; GLFV dehydrog N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ418037; CAD10750.1; -. HSSP; P96110; 1B26.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nguyen H.V.;
"New S. past
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACT_SITE
   SUBUNIT: Arylphorin is a hexamer of subunits alpha and SUBCELLULAR LOCATION: Extracellular. TISSUE SPECIFICITY: Fat body.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: Homohexamer (By similarity)
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Pfam; PF00372; hemocyanin; 1.
Pfam; PF03723; hemocyanin; 1.
Pfam; PF03723; hemocyanin N; 1.
Pfam; PF03722; hemocyanin N; 1.
Pfam; PF03723; hemocyanin N; 1.
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SUMMARIES

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ALIGNMENTS

R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldn A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A;Reference number: A97359; MUID:21608551; PMID:11743194 B ş A; Gene: AGR C 1045
A; Map position: circular chromosome alpha-glucosides-binding periplasmic protein aglE precursor [imported] - Agrobacterium C;Species: Agrobacterium tumefaciens C;Bate: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002 C;Accession: A97431 C; Genetics: A;Residues: 1-453 <K A;Cross-references: A; Molecule type: DNA A; Residues: 1-453 < KUR> A;Status: preliminary A; Accession: A97431 Query Match Best Local S Matches 7 Local Similarity les 7; Conserv 169 DVKSLVWYVPENF 181 DIKQFVWYTPPTF 15 Conservative GB:AE007869; PIDN:AAK86402.1; PID:g1515534; GSPDB:GN00169 51.6%; 1; Score 48; Pred. No. Mismatches В 2 s, Length 453, Indels 0; Agent Agrobacterium Gaps 0; Goldmar

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hypothetical protein aglE [imported] - Agrobacterium tumefaciens (strain C58, Dupont) C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002 C;Accession: AB2649

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordonster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AB2649
A;Status: preliminary R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001 Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm

A; Ducuse type: DNA A;Molecule type: CNR A;Residues: 1-453 <KUR > A;Cross-references: GB:AE008688; PIDN:AAL41608.1; PID:g17738945; GSPDB:GN00186

C;Genetics: A;Gene: aglI A;Map positi

ne: aglE position:

circular chromosome

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R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B. AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A;Title: Distinct populations of human immunodeficiency virus A;Reference number: S70417; MUID:92144209; PMID:1736940
A;Accession: S70425
                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-358 <STE1>
A; Cross-references: EMBL: X61359; NID: g60182; PIDN: CAA43630.1; PID: g60183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W. submitted to the EMBL Data Library, July 1991
A;Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as A;Reference number: S21990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Cottam, G.P.; Moran, D.N
Biochem. J. 234, 305-310,
A;Title: Physicochemical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                allergen R7 - perennial ryegrass (tentative sequence) (fragment)
C;Species: Lolium perenne (perennial ryegrass)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jun-2000
conserved hypothetical protein YPO0524 [imported]
C;Species: Yersinia pestis
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                                                                                                                                                                                                                                                                                   A; Cross-references:
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A; Residues: 1-222, 'X', 224-358 <STE2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: human immunodeficiency virus type 1, HIV-1
A;Variety: isolate 28
C;Darte: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
C;Accession: S21998; S70425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     envelope protein gp120/gp41 - human immunodeficiency virus C;Species: human immunodeficiency virus type 1, HIV-1
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Pred. No. 4.1;
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 A; Experimental source: strain 16M
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C;Accession: AC0065
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarragda, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre Nature 413, 523-527, 2001
                                                                                                                                                                   R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, ; Mazur, M.; Goltsman, E.; Selkov, B.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
                                                                                                                                                                                                                                                                                                          hypothetical membrane spanning protein BMEII0279 [imported] - Brucella melitensis C;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
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C;Superfamily: acetate-CoA ligase; acetate-CoA ligase homology
F;145-621/Domain: acetate-CoA ligase homology <ACL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: E69274
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A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Molecule type: DNA
A;Residues: 1-331 <KUR>
A;Cross-references: GB:AE008918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jan-2000
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                                                                                                                  A;Reference number: AD3252; PMID:11756688 A;Accession: AF3544
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                                                                                   A; Status: preliminary
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53.8%;
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        PIDN:AAL53521.1;
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Pred. No. 20;
1; Mismatches
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Pred. No. 24;
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        PID:g17984427; GSPDB:GN00191
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A; Map position: 4
A; Introns: 160/3;
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                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein Y57G11C.31 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text
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A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J. A;Title: Comparative genomics of Listeria species.

A;Reference number: ABI077; MUID:21537279; PMID:11679669

A;Accession: AH1469
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AH1469
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A; Residues: 1-425 <WIL>
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A; Residues: 1-361 <GLA>
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R;Glaser, P.; Frangeul, L.;
; Dominguez-Bernal, G.; Duc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics:
A; Gene: BMEII0279
                                                                                                                                                                                                                                                                       A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                       R; McMurray, A.
                                                                                                                                                                                                                                                                                                                                                      C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D.; Jones, L.M.; Karst,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     internalin protein homolog lin0295 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
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                                                                                  Matches
                                                                                                Query Match
Best Local
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Best Local
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Best Local
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                     146
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5; Conserv
                                                                                 Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 47.3%;
Similarity 42.9%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                        T27241
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                   WPEIQQFHWPTPSLY 160
                                                 WIDIKQEVWYTPPTE 15
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                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                              187/2; 309/2; 361/3
                                                                                              47.3%;
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chaud, E.; Durand, L.; Dussurget,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    323
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Pred. No. 13;
5; Mismatches
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                                                                                            Score 44; DB
Pred. No. 18;
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Pred.
                                                                                                                                                                                                                                                                                                                       September
                                                                                  Mismatches
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                                                                                                                                                                                                                                                                        GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44;
No.
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                                                                                                             Length 425;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ro, F.; Berche, P.; Bloec
O.; Entian, K.D.; Fsihi,
                                                                                                                                                                                                                                                                                                                                                                     15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-Nov-2001
                                                                             0;
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                                                                               Gaps
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Fsihi, H.
        A;Description: Structural organization of A;Reference number: Z18168
                                       C;Accession: T14669
R;Hu, P.; Elliott, J.; McCready, P. submitted to the EMBL Data Library, submitted to the EMBL Data Library.
                                                                                      C;Species: Yersinia pestis
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
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                                                                                                                          P-loop protein -
                                                                                                                                                         RESULT 12
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                                                                                                                                           T14669
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T14669
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C;Accession: A89958

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Mizutani.Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, ma, A.; Mizutani.Ui, Y.; Kobayashi, N.; Hayashi, H.; Hiramatsu, K. C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Accession: A89958
                                                                                                                                                                             C; Keywords: zinc finger F;932-991/Domain: GATA-type zinc
                                                                                                                                                                                                                                                                                                                                                                                                             R;Ballario, P.; Vittorioso, P.; Magrelli, A.; Talora, C.; Cabibbo, A.; Macino, G. EMBO J. 15, 1650-1657, 1996
A;Title: White collar-1, a central regulator of blue light responses in Neurospora, A;Reference number: S69206; MUID:96203083; PMID:8612589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Neurospora crassa
C;Date: 21-Apr-1997 #sequence_revision 09-May-1997 #text_change 11-Jan-2002
C;Accession: S69206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acetyl-CoA synthetase [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 17-May-2002
                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-1154 < BAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: acsA
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:BA000018; PID:g13701528; PIDN:BAB42822.1; GSPDB:GN00149 A;Experimental source: strain N315
                                                                                                                                                                                                                                                    A; Introns: 967/3
                                                                                                                                                                                                                                                                                             A; Cross-references: EMBL: X94300;
                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S69206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       regulator protein white collar 1 - Neurospora crassa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
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Best Local S
Matches 7
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                                                                                                                                     Query Match
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529 DIGOYIW-TPPT 539
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                                                                                       Similarity
8; Conserv
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                                          DIKQFVWYTPPT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEKUTIWYTAPT 303
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                                                                                       Conservative
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                                                                                                          46.8%;
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•-
                                                                                                                                                                             finger homology
                                                                                                                                                                                                                                                                                          NID:g1279576; PID:g1480115
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                                                                                                             Score 43.5;
Pred. No. 6
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Pred. No.
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                                                                                          Mismatches
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                                                                                                                                     DB
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Yersinia pestis

plasmid pMT1

J.; McCready, P.; Skowronski, E.; Garnes, MBL Data Library, March 1998

virulence

determinants

'n

three Yersinia

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Kobayashi, A.;

Carranc pest

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RESULT 15
S49197
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R;Lindler, L.E.; Plano, G.V.; Burland, V.; Mayhew, G.F.; Blattner, F.R.
Infect. Immun. 66, 5731-5742, 1998
Infect. Immun. 66, 5731-5742, and derailed analysis of the Yersinia pe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-402 <HUP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein Y1030 - Yersinia pestis plasmid pMT1 C;Species: Yersinia pestis C;Date: 20-Sep_1999 #sequence_revision 20-Sep_1999 #text_change 22-Oct-1999 C;Accession: T14946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:AF053947; NID:g2996286; PID:g2996304; PIDN:AAC13184.1
C;Genetics:
                                                                           DЬ
                                                                                                           20
                                                                                                                                                                                                                                 C; Keywords:
                                                                                                                                                                                                                                               A;Cross-references: GB:L02587
C;Superfamily: type E retrovirus env polyprotein
                                                                                                                                                                                                                                                                                       A; Molecule type: genomic RNA
A; Residues: 1-863 < VAN>
                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                             A;Title: Genomic cloning and complete sequence analysis of a highly divergent African hua;Reference number: A53034; MUID:94149849; PMID:8107220
A;Accession: A53034
                                                                                                                                                                                                                                                                                                                                                                                                      R;Vanden Haesevelde, M.; Decourt, J.L.; De Leys, R.J.; Vanderborght, B.; van der Groen, J. Virol. 68, 1586-1596, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: A53034
                                                                                                                                                                                                                                                                                                                                                                                                                                                        gag polyprotein - human immunodeficiency virus type 1 (strain Ant70)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:AF074611; NID:g3883003; PID:g3883031; PIDN:AAC82691.1
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A; Residues: 1-418 <LIN>
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A;Title: Complete DNA sequence and detailed analysis of the Yersinia pestis KIM5 plasmid
A;Reference number: Z18268; MUID:99043898; PMID:9826348
A;Accession: T14946
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Best Local S
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                                                                                                                                                     Matches
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                                                                             672
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                                                                                                                                               46.2%;
Similarity 50.0%;
5; Conservation
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                                                                             WLDITKWLWY 681
                                                                                                               WIDIKQFVWY 10
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                                                                                                                                                     Score 43; DB Pred. No. 57; 4; Mismatches
                                                                                                                                                     4.
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Pred. No. 24;
1; Mismatches
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Pred. No.
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25;
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                                                                                                                                                                                       Length 863;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 402;
                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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A;Experimental source: isolate VAU

(;Superfamily: type E retrovirus env polyprotein; transmembrane protein
C;Keywords: glycoprotein; capsid protein; coat protein; transmembrane protein
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-S55/Product: coat protein gp120 #status predicted <CP1>
F;536-B77/Product: coat protein gp120 #status predicted <CP2>
F;536-B77/Product: coat protein gp121 #status predicted <CPN>
F;598-716/Domain: transmembrane #status predicted <TMN>
F;59,88,139,148,159,184,188,198,230,235,242,263,270,277,292,302,333,345,357,367,396,404,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          envelope protein precursor - human immunodeficiency virus type 1 (fragment) c;Species: human immunodeficiency virus type 1, HIV-1 C;Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 26-Aug-1999 C;Accession: S49197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Charneau, P.; Borman, A.M.; Quillent, C.; Guetard, D.; Chamaret, S.; Cohen, J.; Remy, submitted to the EMBL Data Library, July 1994
A;Description: Isolation and envelope sequence of a highly divergent HIV-1 isolate: defi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-877 < CHA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: S49197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: S49197
                                                                                                                        Matches
                                                                                                                                                 Query Match
Best Local
   686 WLDITKWLWY 695
                                                            μ
                                                                                                                     Similarity 5; Conserv
                                                            WIDIKQFVWY 10
                                                                                                                        Conservative
                                                                                                                                                 46.2%;
                                                                                                                     Score 43; DB Pred. No. 58; 4; Mismatches
                                                                                                                                                                                 2:
                                                                                                                        1:
                                                                                                                                                                             Length 877;
                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PID:g510517
                                                                                                                        0
                                                                                                                     Gaps
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Search completed: July 12, 2004, 14:11:20 Job time: 8.5 secs

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Minimum DB
Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     July 12, 2004, 14:10:33; Search time 26.5116 Seconds (without alignments) 176.480 Million cell updates/sec
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93
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/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1279676
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	UMMARIES	
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,	93	100.0	15	14	US-10-011-095-21	Sequence
	93	100.0	15	14	US-10-011-095-21	
N	93	100.0	15	14	US-10-010-667A-21	-
ω	93	100.0	15	14	US-10-165-044-39	
4	93	100.0	267	9	US-09-747-835A-50	
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œ	93	100.0	339	9	US-09-759-143-879	φ
9	93	100.0	339	φ	US-09-780-669-879	φ
10	93	100.0	339	9	US-09-822-827-879	φ
11	93	100.0	339	9	US-09-802-520-11	
12	93	100.0	339	9	US-09-895-793-879	9
13	93	100.0	339	9	US-09-895-814-879	79
14	93	100.0	339	12	US-10-205-267-13	ω
15	93	100.0	339	12	TIS-10-408-009-3	

45	44	43	42	41	40	39	38	37	36	3 5	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
43	43	43	43	43	44	44	44	44	44	44	44	44.5	44.5	45	45	45	45	45	93	93	93	93	93	93	93	93	93	93	93
46.2		o		9	47.3	47.3	47.3	47.3	47.3	47.3	47.3	47.8	47.8	α	48.4	48.4	48.4	48.4	100.0	100.0	•	100.0	100.0		•	100.0	100.0	100.0	100.0
147	119	98	89	71	568	568	568	403	103	91	70	662	553	871	854	483	269	268	375	368	339	339	339	339	339	339	339	339	339
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US-09-873-134-2	S-10-25	US-10-424-599-193800	-10-05	37-	-10-	US-09-815-242-12629	242-549	US-10-301-997-83	US-10-437-963-172139	US-10-424-599-232688	US-10-437-963-139012	0-369-	US-10-282-122A-77905	US-10-346-000A-9	US-10-369-294-17	US-10-282-122A-57398	US-09-854-816-33	3	US-10-165-044-2	US-10-425-114-72779	US-10-295-027-1347	95-027	US-10-239-607-37	US-10-294-025-879	US-10-144-678A-879	US-10-205-823-397	US-10-010-667A-2	US-10-011-095-2	US-10-012-896-879
Sequence 2, Appli	Sequence 41, Appl	193	62	115	e 44	12629,	5492	80	Sequence 172139,		13901			Sequence 9, Appli		(D			Sequence 2, Appli		134	714	Sequence 37, Appl	879	e T	39	e 2,	Sequence 2, Appli	Sequence 879, App

ALIGNMENTS

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PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 15
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                              S
                                                                                                                                          ; OTHER INFORMATION: STEAP-1 PEPTIDE US-10-011-095-21
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                                                                    Query Match
Best Local S
Matches 15
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Publication No. US20030045682A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Saffran, Douglas C.
APPLICANT: Mitchell, Steve Chappell
TITLE OF INVENTION: ANTIBODIES IMMUNOSPECIFIC FOR STEAP1 (AS AMENDED)
FILE REFERENCE: 511582001610
CURRENT APPLICATION NUMBER: US/10/011,095
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 09/323,873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Afar, Daniel APPLICANT: Hubert, Ren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                              FEATURE:
                      1 WIDIKQFVWYTPPTF 15
1 WIDIKQEVWYTPPTF 15
                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hubert, Rene
Leong, Kahan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Raitano, Arthur B.
                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rene S.
                                                                                     100.0%;
                                                                      0;
                                                                    Score 93; DB 14;
Pred. No. 2.2e-07;
Mismatches 0;
                                                                                                      DB 14; Length 15;
                                                                      Indels
                                                                    0;
                                                                    Gaps
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US-10-010-667A-21

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US-10-165-044-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 15
TYPE: PRT
CRGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Publication No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21, Application US/10010667A Publication No. US20030055217A1 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 511582001601
CURRENT APPLICATION NUMBER: US/10/010,667A
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILING DATE: 1999-06-01
                                                                                                                                                                                                                                                                                           APPLICANT: Aya Jakobovits
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 51158-20016.02
CURRENT APPLICATION NUMBER: US/10/165,044
CURRENT FILING DATE: 2002-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Arthur B. Raitano
APPLICANT: Douglas Saffran
APPLICANT: Daniel E.H. Afar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
                                           PRIOR APPLICATION NUMBER: US 09/455,486
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: WO 99/62941
PRIOR FILING DATE: 1999-06-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Agensys, Inc.
APPLICANT: Rene S. Hubert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Raitano, Arthur B.
APPLICANT: Saffran, Douglas C.
APPLICANT: Witchell, Steve Chappell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Afar, Daniel
APPLICANT: Hubert, Rene S.
APPLICANT: Leong, Kahan
                                                                                                                                            PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 09/323,873
PRIOR FILING DATE: 1999-06-01
                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: US 60/091,183
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
FILING DATE:
                      APPLICATION NUMBER: PCT/US00/33040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/10165044
No. US20030149531A1
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mary Faris
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Steven Chappell Mitchell
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2000-12-06
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GENERAL INFORMATION:

APPLICANT: Yamazaki, APPLICANT: Tang, Y.

Victoria

APPLICANT:

Tang, Y. Tom Liu, Chenghua

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; Sequence 51, Application US/09747835A
; Patent No. US20020146692A1
                                      US-09-747-835A-51
                                                     RESULT 5
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                                                                                                                                                                                                                                                            US-09-747-835A-50
                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: US 09/653,450
PRIOR APPLICATION NUMBER: US 09/620,312
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US 09/598,042
PRIOR PILING DATE: 2000-07-19
PRIOR PILING DATE: 2000-06-20
PRIOR PILING DATE: 2000-06-20
PRIOR PILING DATE: 2000-04-25
PRIOR PILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR PILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 63
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                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.0 SEQ ID NO 50 LENGTH: 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 50 Patent No.
                                                                                                                                                                                   Matches
                                                                                                                                                                                                 Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ren, Feiyan
APPLICANT: Asundi, Vinod
APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIKE
TITLE OF INVENTION: LIKE) POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: HYS-37CIP
CURRENT PILLING DATE: 2002-03-08
CURRENT FILLING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: US 09/729,739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Yamazaki, Vici
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                           211 WIDIKQFVWYTPPTF 225
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). US20020146692A1
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Liu, Chenghua
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Wang, Dunrui
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Pred. No. 2.2e-07;
                                                                                                                                                                                                     Score 93; DB 9;
Pred. No. 3.3e-06;
                                                                                                                                                                                   Mismatches
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APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Ren, Feiyan
APPLICANT: Lymanac, Radoje T
ITILE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIKE
ITILE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIKE
ITILE OF INVENTION: LIKE) POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: 21272-015-061/HYS-37CIP
CURRENT APPLICATION NUMBER: US 09/1312,312
CURRENT FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: US 09/53,450
PRIOR APPLICATION NUMBER: US 09/653,450
PRIOR APPLICATION NUMBER: US 09/653,450
PRIOR APPLICATION NUMBER: US 09/653,450
PRIOR APPLICATION NUMBER: US 09/653,312
PRIOR APPLICATION NUMBER: US 09/650,312
PRIOR APPLICATION NUMBER: US 09/650,312
PRIOR APPLICATION NUMBER: US 09/552,317
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CURRENT APPLICATION NUMBER: US/09/747,835A
CURRENT FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: US 09/729,739
PRIOR APPLICATION NUMBER: US 09/653,450
PRIOR PRILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US 09/653,450
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US 09/620,312
PRIOR APPLICATION NUMBER: US 09/598,042
PRIOR APPLICATION NUMBER: US 09/598,042
PRIOR APPLICATION NUMBER: US 09/598,042
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
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APPLICANT: Ren, Feiyan
APPLICANT: Asundi, Vinod
APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: METHODS AND MATERIAL
TITLE OF INVENTION: LIKE) POLYPEPTIDES
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR FILING DATE: 2000-04-25
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Liu, Chenghua
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No. US20040068097A1
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Dunrui
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AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES
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PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US 09/620,312
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US 09/598,042
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
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Sequence 879, Application Patent No. US20020022248A1
                                                                                                                                                                                                                                                                                                        SOFTWARE: P
SEQ ID NO 51
                                                                                                                                                                                    Query Match
Best Local (
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Best Local Similarity
                                                                                                                                                                      Matches
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APPLICANT:
APPLICANT:
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PRIOR APPLICATION NUMBER: US 09/729,739
PRIOR FILING DATE: 2000-12-04
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APPLICANT: Ren, Feiyan
APPLICANT: Ren, Feiyan
APPLICANT: Asundi, Vinod
APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIE
TITLE OF INVENTION: LIKE) POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: 21272-015-061/HYS-37CIP
                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 63
                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 2000-01-21
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                                                                                                                                                                                                                                                                         TYPE:
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TYPE: PRT
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PRT
                                                                                                    211 WIDIKOFVWYTPPTF 225
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                                                                                                                         WIDIKQFVWYTPPTF 15
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Liu, Chenghua
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No. US20040068097A1
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Wang, Dunrui
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Tang, Y. Tom
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                 US/09759143
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GENERAL INFORMATION:

APPLICANT:

Xu, Jiang Dillon, I Mitcham,

Jiangchun llon, Davin C. cham, Jennifer

APPLICANT:

Harlocker, Susan L. Jiang, Yuqui

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; SOFTWARE: FASTSEQ for Wi
; SEQ ID NO 879
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-780-669-879
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US-09-780-669-879
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 879
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Patent No. US20020051977A1
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APPLICANT:
APPLICANT:
                                                                                                                                    APPLICANT: Skeik, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
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CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
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APPLICANT:
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APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
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                                                                                                     CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 100.0%; Score 93; DB 9; Local Similarity 100.0%; Pred. No. 4.2e-06;
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                                                                                       FastSEQ for Windows Version 3.0
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Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
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Retter, Marc W.
Stolk, John A.
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Kalos, Michael D.
Fanger, Gary R.
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Kalos, Michael D.
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Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitcham, Jennifer L.
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                                                                                                                                                                                                                                                                                                    Wang,
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                                                                                                                                                                                                                                                                                                                     Li, Samuel
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                                                                                                                                                                                                                                                                                                 Aijun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Susan L.
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APPLICANT: Faris, Mary
APPLICANT: Chen, Huei-Mei
APPLICANT: Chen, Huei-Mei
APPLICANT: Ison, Craig H.
TITLE OF INVENTION: STEAP-RELATED PROTEIN
FILE REFERENCE: PC-0037 US
CURRENT APPLICATION NUMBER: US/09/802,520
CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PERL Program
SEQ ID NO 11
LENGTH: 339
TYPE: PRI
COCCURENT OF SEX O
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-822-827-879
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US-09-822-827-879
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                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020187472A1 g6572948
US-09-802-520-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
US-09-802-520-11
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APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/09802520 Publication No. US20020187472A1 GENERAL INFORMATION:
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Patent No. US20020081680A1
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Best Local Similarity
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Best Local Similarity 100.0%;
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Best Local Similarity
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277 WIDIKOFVWYTPPTF 291
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                                            1 WIDIKQEVWYTPPTF 15
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100.0%; Pred. No. 4.2e-06;
                                                                                                                                                                       100.0%; Score 93; DB 9;
100.0%; Pred. No. 4.2e-06;
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Pred. No. 4.2e-06;
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RESULT 12 US-09-895-793-879

Sequence 879, A Publication No.

Application US/09895793 o. US20020192763A1

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APPLICANT:
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APPLICANT:
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C2
CURRENT FILLOR DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
NUMBER OF SEQ ID NOS: 982
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FASTSEQ for Windows Version 3.0
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APPLICANT:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennife
APPLICANT: Harlocker, Susan
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ORGANISM: Homo sapiens
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                                                                                                                                   Retter, Mar.
Retter, Mar.
Retter, Mar.
Retter, Mar.
Retter, Mar.
Stolk, John A.
Day, Craig H.
Day, Craig H.
Thomas S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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Dillon, Davin C.
Mitcham, Jennifer L.
McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
Foy, Teresa
                                                                 Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
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Houghton, Raymond L.
Vinals de Bassols, Carlota
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Kalos, Michael D.
                                                                                                                                                                                                                   Jiang,
                                                                                                                                                                                                                                   Harlocker,
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Stolk, John J
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                                                       Hural, John
                                                                                                            Wang,
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Hepler, William T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                         Samuel X.
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ick, Thomas S.
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                                                                                                           Aijun
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Pred. No.
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GENERAL INFORMATION:
APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Arthur B. Raite
APPLICANT: Douglas C. Saff
APPLICANT: Stephen C. Mitc
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US-10-408-009-2
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SOFTWARE: PERL Program
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/10205267 Publication No. US20030064397A1 GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 879
                                                                                                                                                                                                                                                                     Sequence 2, Application US/10408009 Publication No. US20040072196A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
APPLICANT: Rene S. Hubert
APPLICANT: Arthur B. Raltano
APPLICANT: Douglas C. Saffran
APPLICANT: Stephen C. Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THE
FILE REFERENCE: 511582001603
CURRENT APPLICATION NUMBER: US/10/408,009
CURRENT FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 09/455,486
PRIOR FILING DATE: 1999-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Spancake, Kimberly M.
APPLICANT: Rickert Paula K.
APPLICANT: Lal, Preeti G.
APPLICANT: Ison, Craig H.
TITLE OF INVENTION: TRANSMEMBRANE
TITLE OF INVENTION: TUMORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PILLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank ID No:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2002-07-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: PV-0008 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 339
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; PRIOR APPLICATION NUMBER: 09/323,873
; PRIOR FILLING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 339
; TYPE: PRI
; ORGANISM: Homo sapiens
US-10-408-009-2

Query Match
Best Local Similarity 100.0%; Score 93; DB 12; Length 339;
Best Local Similarity 100.0%; Pred. No. 4.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Search completed: July 12, 2004, 14:27:49

Search completed: July 12, 2004, 14:27:49

Job time: 26.5116 secs
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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DB
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length: 2000000000
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Match
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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1 WIDIKQFVWYTPPTF 15
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       GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
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   US-09-323-873A-21

US-09-323-873A-2

US-09-685-166A-879

US-08-965-056-39

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US-08-965-056-39

US-08-118-270-45

PCT-US93-08528-45

PCT-US93-08528-45

PCT-US93-08528-45

US-09-134-000C-4888

US-09-134-000C-4888

US-09-134-031-13

US-08-472-240A-8

US-08-817-441-83

US-08-817-441-1102

US-08-817-441-1102

US-08-965-056-71

US-08-965-056-71

US-08-965-056-71

US-08-965-056-73

US-08-381-532A-7241

US-08-381-531-642

US-08-448-489-11

US-08-448-489-11

US-08-448-489-11

US-08-448-489-11

US-08-488-351B-642

US-08-965-056-73

US-08-965-056-73
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Sequence 21, Appli Sequence 2, Appli Sequence 39, Appli Sequence 39, Appli Sequence 45, Appli Sequence 45, Appli Sequence 17, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 14, Appli Sequence 61, Appli Sequence 68, Appli Sequence 71, Appli Sequence 71, Appli Sequence 71, Appli Sequence 68, Appli Sequence 7241, Appli Sequence 642, Appli Sequence 64, Appli
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RESULT 2
US-09-323-873A-2
; Sequence 2, Application US/09323873A
; Patent No. 6329503
; GENERAL INFORMATION:

APPLICANT: Daniel E. Afar APPLICANT: Rene S. Hubert APPLICANT: Kahan Leong APPLICANT: Arthur B. Raitano APPLICANT: Douglas C. Saffran APPLICANT: Steve Chappell Mitchell

Query Match Best Local Matches 1 Qy 1 Db 1	323 323 CHARLE CARRETTICS CARRED CARRETTICS	RESULT 1	22 C C C C C C C C C C C C C C C C C C
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Score 93; DB 4; Le Pred. No. 3.5e-08; 0; Mismatches 0;	3873A hell NTINE TRANSMEMBRANE IN HUMAN CANCERS ANI 09/323,873A 1,7,520 1,183 1,183 1,183 17,520 1,183	ALIGNMENTS	US-08-965-056-13 US-08-965-056-14 US-08-965-056-72 US-08-965-056-22 US-08-965-056-25 US-08-965-056-25 US-08-965-056-25 US-08-965-056-25 US-08-965-056-67 US-08-471-770-46 US-08-471-770-46 US-09-886-156-46 US-09-886-149-46 US-09-886-149-46 US-09-886-1150-46
15; ls 0;	ANTIGENS) USES THEREOF		Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence
Gaps 0;			13, Appl 14, Appl 70, Appl 71, Appl 21, Appl 22, Appl 22, Appl 37, Appl 46, Appl

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RESULT 4
US-08-965-056-39
; Sequence 39, Ap
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APPLICANT: Dillon, Davin
APPLICANT: Mitcham, Jenni
APPLICANT: Harlocker, Sus
APPLICANT: Jiang, Yuqui
                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 898
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 879
LENGTH: 339
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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LENGTH: 339
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PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
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                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.427C21 CURRENT APPLICATION NUMBER: US/09/685,166A CURRENT FILING DATE: 2000-10-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
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Local Similarity 100.0%;
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                                                                                         WIDIKQFVWYTPPTF 291
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 Application US/08965056
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Carter, Darrick
Li, Samuel
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ick, Thomas S.
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100.0%; Pred. No.
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Pred. No.
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                                                                                                                                                                                                                                                                      Patent No. 6271198
GENERAL INFORMATION:
APPLICANT: Andrew
                                                                                                                                                                                                                                                                                                                    Sequence 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
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APPLICANT: Andrew
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APPLICANT: James A.
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
                                                                                                                             NUMBER OF SEQUENCES: 1
                                                                                                                                                          TITLE OF INVENTION: Constrained TITLE OF INVENTION: Making Same
                                                                                                                                                                                          APPLICANT:
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                                                                STREET: 1 DNA Wa
CITY: South San
STATE: Californi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/965,056 FILING DATE: 05-No. 6271198-1997 CLASSIFICATION: 530
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                                               COUNTRY:
                                                                                                              ADDRESSEE:
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Similarity 60.0%;
6; Conservative
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Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasnik
                                                                                                                                                                                        Melissa A. Starovasnik
James A. Wells
                                                                                                                                                                                                                                      J. Kevin Judice
Robert S. McDowell
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                                                 USA
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                                                                                                                                                                                                                                                                       Andrew C. Braisted
                                                                                                           Genentech, Inc
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                                                                                Francisco
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                                                                                                                                                                           Constrained Helical Peptides and Methods of
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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17;
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SOFTWARE: WinPatin (Ge CURRENT APPLICATION DATA:

COMPUTER: IBM PC OPERATING SYSTEM:

IBM PC compatible SYSTEM: PC-DOS/MS-DOS

(Genentech)
(TA:
US/08/965,056

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RESULT 6
US-08-118-270-45
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                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE

COMPATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Ve:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/118,270

FILING DATE: 09-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/943,236

FILING DATE: 10-SEP-1992
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                         SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acid
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                                                                                                                                          REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MU
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R:
TELECONMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEPAX: 650/952-9881
                                                                                               TELEFAX: 248633
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ADDRESSEE: BROWDY AND NEIMARK
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ATTORNEY/AGENT INFORMATION:
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TOPOLOGY:
                         STRANDEDNESS:
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                                                                                                                                                                                                            Townsend, Kevin G.
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Amino Acid
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Pred. No. 17;
2; Mismatches
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           GENERAL INFORMATION:
APPLICANT: LYMN DOMECTTE-Stamm et al
APPLICANT: LYMN DOMECTTE AT AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FABCALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
                                                                                              Patent No.
                                                                                                Sequence 4888, Application US/09134000C Patent No. 6617156
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CURRENT APPLICATION NUMBER: US/09/134,000C
                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: 202-628-5197
TELEFAX: 202-737-3528
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TITLE OF INVENTION: RECEPTIOES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
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CITY: Washington
CTATE: D.C.
TTATE: TTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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419 Seventh Street, N.W., Suite 300
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Pred. No. 22;
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US-07-956-483-13
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SEQ ID NO 4888
LENCTH: 489
TYPE: PRT
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SEQ ID NO 17
LENGTH: 854
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-09-134-000C-4888
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PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Georges-Courbot, Marie Claude
APPLICANT: Lu, Chang Yong
TITLE OF INVENTION: Complete Genome Sequences of a Simian
TITLE OF INVENTION: Immunodeficiency Virus from a Red-Capped
TITLE OF INVENTION: Mangabey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hahn, Beatrice H. APPLICANT: Gao, Feng APPLICANT: Marx, Preston A.
                                                                                                                               GENERAL INFORMATION:
APPLICANT: KIENY, Marie-Paule
TITLE OF INVENTION: NOVEL HYBRID, SOLUBLE AND UNCLEAVED
TITLE OF INVENTION: 9p160 VARIANT
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Shaw, George M.
APPLICANT: Smith, Stephen M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/206,551B
CURRENT FILING DATE: 1998-12-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Simian immunodeficiency virus FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Amino acid sequence of homologous region of OTHER INFORMATION: SIVcpzANT lentiviral env protein
                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 60.0%; hes 6; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 6; Conserv
STATE: Virginia COUNTRY: United States ZIP: 22313-1404
                                                       STREET: P.O. Box CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE: D6286
                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  450 WPEITQIIWLAPP 462
                                                                                                                                                                                                                                                                                                                                                  670 WEDITQWLWY 679
                                                                                                                                                                                                                                                                                                                                                                                      1 WIDIKQFVWY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WIDIKQEVWYTPP 13
                                                                           E: Burns, Doane, Swecker & Mathis P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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46.2%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45; DB Pred. No. 54;
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REFERENCE/DOCKET NUMBER: 0177;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEPAX: (703) 836-2021;
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 865 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-07-956-483-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application Patent No. 6284248
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local
                                                                                                                                      ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,240A
FILING DATE: 07-UN-1995
CLASSIFICATION: 435
              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/956
PILING DATE: 31-DGC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 0177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FR 91 05392 FILING DATE: 02-MAY-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 12-NOV-1 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 31-DEC CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE: 12-NOV-1992
                                                                                                                                                                                                                                                                                                                                         STREET: F. CTTY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                        STATE: Virginia COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 681 WEDITQWLWY 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 WIDIKQFVWY 10
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                                                                                                          US 07/956,483
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                    017753-055
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Pred. No.
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Query Match
Best Local Similarity
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RESULT 13
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US-08-887-534A-83
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GENERAL INFORMATION:
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TELEX: (312) 474-6600
INFORMATION FOR SEQ ID NO:
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 887 amino acids
TYPE: amino acids
                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 403 amino acids
                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 28.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: US/08/887,534A
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Holden, TITLE OF INVENTION: NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION:
                                                                                                                                                                                                                                                                                                                                       NAME:
                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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Local Similarity 60.0%;
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STRANDEDNESS: not
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                                       305 DEKVTIWYTAPT 316
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                                                                 DIKQFVWYTPPT 14
                                                                                                                                                                                            amino acid
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: United States
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 South Wacker
                                                                                             Conservative
                                                                                                                                                                                                                                                               (312) 474-0448
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                                                                                                         47.3%;
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ANTI-BACTERIAL METHODS AND MATERIALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106
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cker Drive/6300 Sears Tower
                                                                                                                                                                                                                                   83:
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                                                                                    Pred. No. 30;
1; Mismatches
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                                                                                                                                                                                                                                                                                                       28341/33996
                                                                                                                   Score 44;
                                                                                                                    DB 4; Length 403;
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                                                                                         Indels
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RESULT 14
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                                                                                                                                                                                                            ; Patent No. 6399294; GENERAL INFORMATION:
; APPLICANT: CHARNEA!
; APPLICANT: CLAYEL,
; APPLICANT: BORMAN,
                                                                                                                                                                                                                                                                                                       US-08-817-441-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-527-431-83
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                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: (312) 474-6600 INFORMATION FOR SEQ ID NO:
                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                   APPLICANT:
                                                                           CORRESPONDENCE ADDRESS:
                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Holden, David W.
TITLE OF INVENTION: ANTI-BACTERIAL METHODS AND MATERIALS
NUMBER OF SEQUENCES: 106
                                 STREET:
                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                305 DEKVTIWYTAPT 316
                                                                                                                                                                                                                                                                                           47,
Washington DC
                                                                                                                                                                                                                                                                                                                                                                                              3 DIKOFVWYTPPT 14
                                                                                                                                                                                                                                                                             ', Application US/08817441
6399294
                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60606
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                             1300 I Street, N.W.
                                                                                                                                                                                CLAVEL, FRANCOISE
BORMAN, ANDREW
QUILLENT, CAROLINE
GUETARD, DENISE
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                                                                                                                                    MONTAGNIER, LUC
DONJON DE SAINT-MARTIN, JACQELINE
COHEN, JAQUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (312) 474-0448
                                                                                                                                                                                                                                           CHARNEAU, PIERRE
                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                United States of America
                                             Finnegan, Henderson, Farabow, Garrett Dunner, L.L.P.
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                                                                                                   NUCLEOTIDE SEQUENCES OF HIV-1 TYPE SUBTYPE) ANTIGENS
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                                                                                           103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28341/33996
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 403;
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APPLICANT: Marx, Preston A.
APPLICANT: Shaw, George M.
APPLICANT: Smith, Stephen M.
APPLICANT: Smith, Stephen M.
APPLICANT: Georges-Courbot, Marie Claude
APPLICANT: Iu, Chang Yong
TITLE OF INVENTION: Complete Genome Sequences of a Simian
TITLE OF INVENTION: Immunodeficiency Virus from a Red-Capped
TITLE OF INVENTION: Mangabey
FILE REFERENCE: D6286
CURRENT APPLICATION NUMBER: US/09/206,551B
CURRENT APPLICATION NUMBER: US/09/206,551B
CURRENT FILING DATE: 1998-12-07
NUMBER OF SEQ ID NOS: 58
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-09-206-551-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                   FEATURE:
OTHER INFORMATION: Amino acid sequence of homologous region of OTHER INFORMATION: O_ANT70 lentiviral env protein US-09-206-551-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COURTENT APPLICATION NUMBER: PCT/FR 95/01391
FILING DATE: 11-UTL-1997
PRIOR APPLICATION NUMBER: PCT/FR 95/01391
FILING DATE: 20-OCT-1995
PRIOR APPLICATION NUMBER: FR 941254
FILING DATE: 20-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9502526
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 50.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15, Application US/09206551B Patent No. 6521739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202-408-4400 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hahn, Beat APPLICANT: Gao, Feng
                                                                                                                                                      LENGTH: 862
TYPE: PRT
ORGANISM: Simian immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03260.6005-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Meyers, Kenneth J. REGISTRATION NUMBER: 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 WLDITKWLWY 169
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        46.2%; Score 43;
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        DB 4; Length 862;
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Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps

Qy 1 wIDIKQFVWY 10

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Db 671 WIDITKWIWY 680
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Search completed: July 12, 2004, 14:12:24 Job time : 9.24419 secs

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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
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DB
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length: 2000000000
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                                                                                                              A_Geneseq_29Jan04:*
1: geneseqp1980s:*
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93
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                                                           geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:*
             geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:*
geneseqp2004s:*
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Pred. No. d. No. is the number of results predicted by chance to have a re greater than or equal to the score of the result being printed, is derived by analysis of the total score distribution.

No.

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Abu57721 Human imm	٠ (2 650 TD	1010 Human n	9 Kidney	2790	9829 Himan	4329 Himan	5573 DYORT	DEDECTA CELEBY	Abreadon Drogtot	0114 010M2-1	NOVET III	0		7 Finan D7		8845 Himan	9927 Himan	1282 57995	819	OBB7 Hyman	DARK HIMEN CO.	02788 84141		cription			

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ABP68678	ABM40499	AAU43980	ABM/1219	ADVICES	ARITI 6200	AAU37036	AAU33996	AAW97719	AA004068	ABU49981	101.304	BB037494	AAP80966	AAW43074	AAB69345	ABU294/4	30170040	AAWOOKOK	AAR48724	ABU57715	ABG68308	AAI 2283/	3 170001
		Aau43980 Propionib	Abm71219 Staphyloc	Abul6298 Protein e	_				-	Abu49981 Protein e	Aao27484 Simian im			HTV-1		Abu29474 Protein e	Hawuzbyb G-protein				Envelor	Aay22837 SEO ID NO	

peptide; 15 AA

ALIGNMENTS

AAY58200;

14-MAR-2000

(first entry)

AAY58200 standard;

Synthetic. Serpentine transmembrane antigen of the prostate; STRAP-1; prostate; transmembrane domain; type IIIa membrane protein; expression; cancer; prostate cancer; bladder cancer; colon cancer; pancreatic cancer; ovarian cancer; tumour antigen; immunisation; immune response; cellular; humoral; anticancer vaccine; antibody; detection; diagnosis; prognosis; WO9962941-A2 Homo monitoring; susceptibility; therapeutic inhibitor; drug targetting; recombinant protein. Human STRAP-1 peptide, corresponding to STRAP-1 extracellular region sapiens. ω

RESULT 1
AAY58200
ID AAY58200
ID AAY58200
ID AAY58200
AC AAY5
XX AAY5
XX AAY5
XX Serp
XX Serp
KW Serp
KW Covar
KW Irean
KW Pross
KW Ovar
KW ING
KW Pross
KW OVAR
KW PO99
IX O09-II
XX HORO
PF 01-J
XX O1-J
XX WPI; 2000-072832/06. (UROG-) (AFAR/) (HUBE/) Afar DE, (LEON/) (RAIT/) (SAFF/) 01-JUN-1998; 30-JUN-1998;) AFAR D E.
) HUBERT R S.
) LEONG K.
) RAITANO A B.
) SAFFRAN D C. UROGENESYS INC. Hubert RS, 98US-0087520P. 98US-0091183P. Leong × Raitano ₽В, Saffran

g

01-JUN-1999; 09-DEC-1999

99WO-US012157.

Novel proteins useful as diagnostic particularly for prostatic cancer. markers and therapeutic targets,

Disclosure; Page 22; 83pp; English.

Abg68314 Envelope Abu57721 Human imr

Sequences AAY58198-Y58200 represent synthetic peptides that correspond the extracellular regions of STRAP-1 (serpentine transmembrane antigen o to

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RESULT 2
AABC2788
ID AABC3
AC AABC
XX AABC
XX AABC
XX AABC
XX AABC
DT 06-1
CXX Hums
XX Hums
XX Hums
XX Chrx
XX Chrx
XX Chrx
XX Chrx
XX OChr
XX OCh
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XX OCh
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            agents, to produce anticancer vaccines and to generate specific antibodies. The antibodies may be used for detection, prognosis, and monitoring of cancers (or susceptibility to cancer), as therapeutic inhibitors or to target therapeutic agents to their site of action. STRN nucleic acids may be used for recombinant protein production, as diagnostic and prognostic reagents, for identifying STRAP-expressing cells for screening inhibitors of STRAP expression and for therapeutic modulation/inhibition of STRAP expression. Since high levels of STRAP proteins are exposed on the cell surface, they are easily targetted by systemically administered agents, and because they are expressed mainly on prostatic epithelial cells, agents targetted to them should have minimal side effects on other tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homology to known human proteins. The STRAP-1 gene has been localised to chromosome 7p22. STRAP-1 is thought to be a type IIIa membrane protein and is expressed predominantly in prostate cells in normal human tissues. Structurally, STRAP-1 is a 339 amino acid protein characterised by six
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the prostate, AAY58194). These peptides were used to raise monoclonal anti-STRAP-1 antibodies. STRAP-1 is the prototype member of the STRAP family of proteins (AAY58194-Y58197) which exhibit a high degree of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     structural conservation, but which show no significant structura
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          six transmembrane epithelial antigen of the prostate-1; STEAP-1; chromosome 7p22.3; cancer; prostate; colon; bladder; pancreatic; ovarian; lung; extracellular loop; serpentine transmembrane antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cytostatic; antiproliferative; vaccine; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Extracellular loop #3 of human STEAP-1, suitable for cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE02788 standard; peptide; 15
                                                                                                                                                       06-DEC-1999;
                                                                                                                                                                                                                06-DEC-2000; 2000WO-US033040.
                                                                                                                                                                                                                                                                               07-JUN-2001
                                                                                                                                                                                                                                                                                                                                        WO200140276-A2
                                                                                        (UROG-) UROGENESYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15;
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   Hubert RS,
Jakobovits A;
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                                                                                                                                                       99US-00455486
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                                     Raitano AB,
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Pred. No.
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                                         Saffran DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.5e-07;
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                                            Mitchell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
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10-OCT-2002

2000US-00747835 2000US-00488725 2000US-00552317.

(YAMA/)

YAMAZAKI V.

20-JUN-2000; 19-JUL-2000; 21-JAN-2000; 25-APR-2000; 21-DEC-2000;

2000US-00598042. 2000US-00620312. 2000US-00653450. 2000US-00729739.

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Comprises administering a vaccine comprises administering to the pastent of killing cells expressing STEAP, comprises administering a vaccine comprises administering a vaccine comprises administering a vaccine comprises administering a vaccine composition to the patient. Treating a vector encoding single chain monoclonal antibody that comprises the contains of the heavy and light chains of the monoclonal antibody that specifically binds to STEAP, such that the vector delivers the specifically binds to STEAP, such that the vector delivers the comprises the comprises chain monoclonal antibody coding sequence to the cancer cells and the encoded single chain monoclonal antibody is expressed the encoded single chain monoclonal antibody is expressed contracellularly. The present sequence is extracellular loop of STEAP-1 contracellularly. The present sequence is extracellular loop of STEAP-1 contrable for cloning into pFc, which is used in the invention. STEAP-1 contrable is located on chromosome 7p22.3
В
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-367804/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15
                                                                                                                                                                                                                                                                                                                  Human; G protein-coupled receptor; GPCR; receptor; ophthalmic disease; neurological disease; immunological disease; nephritic disease; cancer; hormonal dysfunction; neoplasm; atherosclerosis; diabetes; chemotherapy; anaemia; irradiation; erythroid precureor; erythroid cell; ulcer; organ; pressure ulcer; vascular insufficiency; surgical wound; traumatic wound; pancreas; liver; intestine; kidney; skin; endothelium; skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU60886 standard; protein; 267 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-MAY-2003
                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                    smooth muscle; cardiac muscle; vascular
                                                                                                                                                                                                                                     US2002146692-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                     G protein-coupled receptor-related (GPCR-related) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention relates to human six transmembrane epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 epithelial antigen of the prostate) cancers, useful for detecting and treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 93; DB 4;
Pred. No. 6.5e-07;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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RESULT 4
ABUGO887
ID ABUG
XX ABUG
XX ABUG
XX Huma
XX H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to treat hormonal dysfunction, cancer and other neoplasia, atherosclerosis, diabetes, in treating various anaemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells. The sequences may be used to promote better or faster closure of non-healing wounds, including pressure ulcers, ulcers associated with vascular insufficiency and surgical and traumatic wounds and in generation or regeneration of other endothelium), muscle (smooth, skeletal, or cardiac) and vascular tissue or for promoting the growth of cells comprising such tissues. Sequences ABU60884-ABU60895 represent human GPCR-related proteins of the invention
                                                                                                                                                                                                                             anaemia; irradiation; erythroid precursor; erythroid cell; chemotherapy; pressure ulcer; vascular insufficiency; surgical wound; traumatic wound; precursor; erythroid cell; ulcer; organ; pressure ulcer; vascular insufficiency; surgical wound; traumatic wound; pancreas; liver; intestine; kidney; skin; endothelium; skeletal muscle; smooth muscle. Cardiac muscle.
                                                                                                                                                                                                                                                                                                                              neurological disease; immunological disease; nephritic
                                                                                                                                                                                                                                                                                                                                                                                                      Human G protein-coupled receptor-related (GPCR-related)
                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human G protein-coupled receptor-like like) proteins and the polynucleotides encoding them. The isola sequences are used for the treatment of diseases of ophthalmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU60887 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamazaki ¹
Asundi V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurological,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   specified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ZHOU/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (RENF/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LIUC/)
                                                                                                                                                                                                                                                                                                                                                G protein-coupled receptor; GPCR; receptor; ophthalmic disease;
                                                                                                                                                                                                                   muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 WIDIKOFVWYTPPTF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REN F.
ASUNDI V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZHOU P.
WANG D.
                                                                                                                                                                                                                                                                                                     dysfunction; neoplasm; atherosclerosis; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZHANG J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WIDIKQFVWYTPPTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polynucleotide for tread nucleotide sequences, mature protein coding I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DRMANAC R T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ۲
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drmanac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunological, or nephritic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; 158pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                              muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for treating, e.g. ophthalmic diseases, quences, or their translated protein cod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ש
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            r translated protein con extracellular portion,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             systems. They may also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhang
                                                                                                                                                                                                                                                                                                                              disease;
                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ç
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                              cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GPCR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       描
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21-DEC-2000; 2000US-00747835.

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RESULT 5
AAY58194
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                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
  Serpentine transmembrane antigen of the prostate; STRAP-1; prostate; transmembrane domain; type IIIa membrane protein; expression; cancer; prostate cancer; bladder cancer; colon cancer; pancreatic cancer; ovarian cancer; thumour antigen; immunisation; immune response; cellular, humoral; anticancer vaccine; antibody; detection; diagnosis; prognosis; monitoring; susceptibility; therapeutic inhibitor; drug targetting;
                                                                                                     Human STRAP-1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                    like) proteins and the polymicleotides encoding them. The isolated sequences are used for the treatment of diseases of ophthalmic, neurological, immunological, or nephritic systems. They may also be to treat hormonal dysfunction, cancer and other neoplasia, atherosclerosis, diabetes, in treating various anaemias or for use i conjunction with irradiation/chemotherapy to stimulate the production crythroid precursors and/or expthroid cells. The sequences may be us promote better or faster closure of non-healing wounds, including pressure ulcers, ulcers associated with vascular insufficiency and
                                                                                                                                   14-MAR-2000
                                                                                                                                                            AAY58194;
                                                                                                                                                                                      AAY58194 standard;
                                                                                                                                                                                                                                                                                                                                                                                   surgical and traumatic wounds and in generation or regeneration of other tissues, e.g. organs (e.g. pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal, or cardiac) and vascular tissue or for promoting the growth of cells comprising such tissues. Sequences ABU60884-ABU60895 represent human GPCR-related proteins of the inventior
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JAN-2000;
25-APR-2000;
20-JUN-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                 Sequence 267 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamazaki V
Asundi V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Fig 4; 158pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     specified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    portion, mature protein
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(LIUC/)
(ZHOU/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ZHAN/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention relates to human G
                                                                                                                                                                                                                                                           211
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                                                                                                                                                                                                                                                                                                              15;
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V, Drmanac RT;
                                                                                                                                                                                                                                                                                                                          Similarity
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TANG Y T.
LIU C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZHOU P.
WANG D.
ZHANG J.
REN F.
ASUNDI V.
                                                                                                                                                                                                                                                        WIDIKQEVWYTPPTF
                                                                                                                                                                                                                                                                                WIDIKQFVWYTPPTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polynucleotide for treating, e.g. ophthalmic diseases, comprise d nucleotide sequences, or their translated protein coding mature protein coding portion, extracellular portion, or active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DRMANAC R
susceptibility; therapeutic protein.
                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 2000US-00488725.

7 2000US-00552317.

7 2000US-0059842.

7 2000US-00620312.

7 2000US-00653450.

7 2000US-00729739.
                                                                                                                                (first entry)
                                                                                                                                                                                      protein;
                                                                                                                                                                                                                                                                                                                          100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
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                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                        Score 93;
Pred. No.
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                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein-coupled receptor-like (GP) otides encoding them. The isolated
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                                                                                                                                                                                                                                                                                                                                      В
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                                                                                                                                                                                                                                                                                                                                  Length 267;
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                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 production
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                                                                                                                                                                                                                                                                                                        0;
                                 cellular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   be used
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                           other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to
                                                                                                                                                                                                                                                                                                       0
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Homo sapiens.

Location/Qualifiers

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This sequence represents a novel human protein, STRAP-1 (serpentine transmembrane antigen of the prostate). STRAP-1 is the prototype member of the STRAP family of proteins (AAYS8194-YS8197) which exhibit a high degree of structural conservation, but which show no significant concluded to chromosome 7p22. STRAP-1 is thought to be a type IIIa conditied to chromosome 7p22. STRAP-1 is thought to be a type IIIa comembrane protein and is expressed predominantly in prostate cells in cormal human tissues. Structurally, STRAP-1 is a 339 amino acid protein cormal human tissues. Structurally, STRAP-1 is a 339 amino acid protein cormal human tissues. Structurally, STRAP-1 is a 339 amino acid protein cormal human tissues. Structurally, STRAP-1 is a 339 amino acid protein cormal human tissues of termini, suggesting that it folds in a "serpentine" manner into three correcellular and two intracellular loops. STRAP-1 mRNA and protein correcellular and two intracellular loops. STRAP-1 mRNA and protein correction of smaintained at high levels and throughout all stages of correction other cancers, including bladder, colon, pancreatic and ovarian cancer. The function of the STRAP proteins is not known. They may be ion cancer. The function of the STRAP proteins is not known. They may be ion cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
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                                                                                                                                                                                                                                                                                       WPI; 2000-072832/06.
N-PSDB; AAZ49395, AAZ49396.
                                                                                                                                                                                                                                                                                                                                                                                         (AFAR/)
(HUBE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1999;
                                                                                                                                                                                                                                                                                                                             Afar DE,
                                                                                                                                                                                                                                                                                                                                                                 (LEON/)
                                                                                                                                                                                                                        Claim 1; Fig
                                                                                                                                                                                                                                                particularly
                                                                                                                                                                                                                                                                                                                                                                                                                   (UROG-)
                                                                                                                                                                                                                                                                                                                                                      (SAFF/)
                                                                                                                                                                                                                                                              proteins useful as diagnostic markers and therapeutic targets
                                                                                                                                                                                                                                                                                                                                                   LEONG K.
RAITANO A B.
SAFFRAN D C.
                                                                                                                                                                                                                                                                                                                                                                                                                   UROGENESYS INC.
                                                                                                                                                                                                                                                                                                                                                                                         AFAR D E.
HUBERT R S.
                                                                                                                                                                                                                                                                                                                             Hubert RS,
                                                                                                                                                                                                                        1A;
                                                                                                                                                                                                                                                  for prostatic cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0087520P.
98US-0091183P.
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                                                                                                                                                                                                                       English.
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RESULT 6
AAMO125
ID AAMO
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DT 04-C
XX HUME
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KW CYTC
XX CYC
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XX I2-C
XX I
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Best Local
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The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) can be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                  New polynucleotide encoding a prostate-specific protein, monitoring and treating prostate cancer in a patient and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-425873/45
                                                                                                                                                                                                                                                                         Claim 2; Page 510-512; 543pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kalos MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Хu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CORI-) CORIXA CORP.
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MD, Fanger GR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Meagher MJ;
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Pred. No. 1.3e-05;
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Retter MW, Stolk JA,
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1, Skeiky
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RESULT 7
AAUG9927
ID AAUG9927
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ID AAUG9927
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XX Huma
OS Homc
XX WO2C
XX O9-W
PR 09-W
PR 13-J
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PR 12-M
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XX YU J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-MAY-2000; 2000US-00570737;
13-UNN-2000; 2000US-00593793;
27-UNN-2000; 2000US-00605783;
09-AUG-2000; 2000US-00636215;
29-AUG-2000; 2000US-00651236;
06-SEP-2000; 2000US-00657279;
02-OCT-2000; 2000US-00679426;
10-OCT-2000; 2000US-00685166;
09-NOV-2000; 2000US-00709729;
            The invention relates to isolated prostate-specific polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate protein, and for inhibiting the development of cancer especially prostate
                                                                                                                                                                                                                                                                                                  New human prostate-specific the diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                              Fanger GR, Reti
Li SX, Wang A,
                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xu J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU69927;
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DB; AAS64160.
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Retter MW,
Skeik
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                                                                                                                                                                                                                                                          Page 549;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Skeiky
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r MW, Stolk JA,
Skeiky YAW, Hepl
                                                                                                                                                                                                                                                   579pp; English.
       comprising the polynucleotide
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                                                                                                                                                                                                                                                                                      polypeptides and polynucleotides useful of cancer, especially prostate cancer.
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Hepler WT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 93;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Harlocker SL, Jiang
A, Day CH, Vedvick T
epler WT, Henderson F
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TS,
RA;
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polypeptide
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RESULT 8

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Matches
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27-APR-2000; 2000US-00560875.
20-UUN-2000; 2000US-00598075.
19-UUL-2000; 2000US-00620325.
01-SEP-2000; 2000US-00654936.
15-SEP-2000; 2000US-00693325.
20-CCT-2000; 2000US-00693325.
30-NOV-2000; 2000US-00728422.
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                                                           The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, haematopolesis regulating activity and may be useful in the diagnosis and/or the properties are activity and may be useful in the diagnosis and/or activity and may be useful in the diagnosis and/or the properties are activity.
treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from to
                                                                                                                                                                                                                                                                                                                  Claim 20;
                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
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7, Zhao QA,
AJ, Yang Y,
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DB; AAK51978.
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J J, Zhang Goodrich R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 93; DB 4; L
Pred. No. 1.3e-05;
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RESULT 9
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(MITC/)
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04-OCT-2000;
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                                                                                                                        Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Moneill PD, Houghton RL, Y De BassolsCV, Foy TM;
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  Prostate specific protein and its encoding polymucleotide, useful for treatment and diagnosis of prostate cancer.
                                                              N-PSDB; ACA59965
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MITCHAM J L.
HARLOCKER S L.
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STOLK J A.
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FOY T M.
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                                                                                                                                                         Kalos MD;
Carter D;
Hural J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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RESULT 10

ABB95387

ID ABB95

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes a fusion protein comprising at least one amino acid sequence of immunogenic portions of any of the 3 sequences not defined in the specification, or sequences having at least 70 or 90 % sequence identity to any one of the 35 sequences defined in the USPTO web site, which is encoded by any of the 4 nucleotide sequences not defined in the specification. The fusion protein, composition and methods are useful for diagnosing, preventing and/or treating cancer, particularly prostate cancer. The proteins are useful as markers to indicate the presence or absence of cancer. This is the amino acid sequence of a presence or absence of cancer. This is the amino acid sequence of a prostate cancer therapy associated protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-FEB-1997;
01-AUG-1997;
10-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seqdata.uspto.gov/sequence.html?DocID=US20020192763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 5;
                                                                                                                                                                                                                                                                                                                                    13-JUL-1999;
12-NOV-1999;
18-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human P789P protein SEQ ID NO 879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB95387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB95387 standard; protein; 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cancer; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUL-2002
                                                                                                                                                                            12-MAY-2000;
13-JUN-2000;
27-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-JAN-2001; 2001US-00759143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                              15-JAN-1999;
09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-JUL-1998;
23-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-FEB-1998;
                                                                                                                                                                                                                                                               09-MAY-2000;
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27-MAR-2000;
                                                                                                                                  29-AUG-2000;
                                                                                                                                                          10-AUG-2000;
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15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; ilarity 100.0%; Conservative
                                                  99US-00443686.

2000US-00536857.

2000US-00568100.

2000US-00568100.

2000US-00593793.

2000US-00605783.

2000US-00636215.

2000US-00651236.

2000US-00657239.

2000US-00657236.

2000US-00657236.

2000US-00657256.
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99US-00288946.
99US-00352616.
99US-00439313.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-00159812.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-00020956.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 93; DB 4; 1
Pred. No. 1.3e-05;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
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ABG61813
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Best Local S
Matches 15
13-OCT-2000;

08-DEC-2000;

08-DEC-2000;

24-JAN-2001;

16-MAR-2001;

16-MAR-2001;

06-APR-2001;

24-APR-2001;
                                                                                                                                                                                                                                                              12-OCT-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG61813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New prostate-specific polynucleot diseases, in particular prostate progression of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG61813 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
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(JIAN/)
(XALO/)
(KALO/)
(FANG/)
(RETT/)
(RETT/)
(STOL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HEND/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (WANG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CART/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEDV/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e present invention provides prostate-specific coding sequences and eair encoded proteins. These can be used in the diagnosis and treatme cancers, particularly prostate cancer. The present sequence is a otein described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ч
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GR, Retter MW, Stolk JA, Day C
Wang A, Skeiky YAW, Hepler WT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WANG A.
SKEIKY Y A W.
HEPLER W T.
HENDERSON R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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RETTER M W.
STOLK J A.
DAY C H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LI S
WANG
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LI S X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DILLON D C.
MITCHAM J L.
HARLOCKER S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer; prostate tumour tissue; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WIDIKQEVWYTPPTF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WIDIKOFVWYTPPTF
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VEDVICK T S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KALOS M D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JIANG
                        ; 2000US-00687576.

2000US-00733288.

2000US-00733748.

2001US-0263957P.

2001US-02768889.

2001US-02768889.

2001US-0281922P.
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      2001US-0286214P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŗ
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Pred.
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A, Day CH, Vedvick T
epler WT, Henderson F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93;
No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosing and
and as markers f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mammal; cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 339;
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TS,
RA;
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Carter D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC The present invention relates to methods of detecting a prostate cancer-
CC contacting a biological sample from the patient with prostate cancer-
CC contacting a biological sample from the patient with prostate cancer-
CC associated polymuclectides (designated PC genes) that selectively
CC hybridise to a sequence that is at least 80% identical to them. The
CC prostate cancer-associated polymuclectide sequences are differentially
CC expressed in prostate tumour tissue or in prostate cancer and are derived
CC from the tissues of various organisms such as humans or other mammals
CC (e.g. mice, sheep and dogs). The methods of the invention are useful for
CC diagnosing and treating prostate cancer in mammals. The prostate cancer
CC associated genes are useful for diagnosing or treating prostate cancer.
CC associated genes are useful for diagnosing or treating prostate cancer.
CC associated genes are useful for diagnosing or treating prostate cancer.
CC associated genes are useful for diagnosing or treating prostate that
CC useful in gene therapy, as a vaccine or in antisense applications.
CC ABG61800-ABG61944 represent prostate cancer-associated proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 15
                  Faris M,
                                                                                                                   06-SEP-2001;
05-APR-2002;
                                                                                                                                                                                              06-SEP-2002; 2002WO-US028371
                                                                                                                                                                                                                                                   20-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                    STEAP-1; six transmembrane epithelial antigen of the prostate; cancer; cancer vaccine; delineation; cytogenetic abnormality; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-JUL-2003
                                                                     (AGEN-) AGENSYS
                                                                                                                                                                                                                                                                                                      WO2003022995-A2
                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                            vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABU98383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABU98383 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 339 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prostate tissue.
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by determining
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04-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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2002US-0370387P
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2001US-0288589P.
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                  Raitano
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein;
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                ΑB,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                339
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Pred. No.
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1.3e-05;
les 0;
          PM,
             Jakobovits
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ttors of PC,
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ABU98414
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention describes a composition comprising a substance that modulates the status of a protein (1) of 340 or 283 amino acids, or of any of the 15 sequences of 259 amino acids, given in the specification, or a molecule that is modulated by the protein, where the status of the cell that expresses the protein is modulated. The compositions, proteins, polynucleotides and methods are useful for treating and detecting cancer. The STEAP-1 related proteins are useful for generating cancer vaccines. The polynucleotides are useful as tools for delineating, with greater precision, cytogenetic abnormalities in the chromosomal region that encodes STEAP-1 that may contribute to the malignant phenotype. This is the amino acid sequence of a variant of human six transmembrane epithelial antigen of the prostate or STEAP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New composition comprising a substance that modulates the status of STEAP-1-related protein, useful for treating and detecting cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABU98414 standard;
                                                                                                                                                                                                                                                            06-SEP-2001; 2001US-0317840P
05-APR-2002; 2002US-0370387P
                                                                                                                                                                                                                                                                                                                                                                                                                                               STEAP-1; six transmembrane epithelial antigen of the prostate; cancer; cancer vaccine; delineation; cytogenetic abnormality; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STEAP-1 variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU98414;
The invention describes a composition comprising a substance that modulates the status of a protein (I) of 340 or 283 amino acids, or any of the 15 sequences of 259 amino acids, given in the specific or a molecule that is modulated by the protein, where the status of the compositions, protein that expresses the protein is modulated. The compositions, protein that expresses the protein is modulated.
                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                           Example
                                                                                                                           STEAP-1-related protein,
                                                                                                                                         New composition
                                                                                                                                                                       WPI; 2003-313240/30
                                                                                                                                                                                                                                 (AGEN-) AGENSYS INC
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DB; ACD02597.
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                                                                                             53; Page 173; 248pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WIDIKQEVWYTPPTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    339 AA;
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                                                                                                                                                                                                   Ge ₩,
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                                                                                                                         comprising a substance that modulates the status of protein, useful for treating and detecting cancer.
                                                                                                                                                                                                     Raitano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.
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Pred. No.
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1.3e-05;
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Best Local Similarity Matches 15; Conserv

100.0%; ilarity 100.0%; Conservative 0

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Score 93; DB 6; Pred. No. 1.3e-05; ; Mismatches 0;

Length 339;

Indels

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Gaps

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Query Match

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RESULT 14
ABU98430
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STEAP-1 variant 8P1D4 v.1
                         The invention describes a composition comprising a substance that modulates the status of a protein (I) of 340 or 283 amino acids, or of any of the 15 sequences of 259 amino acids, given in the specification, or a molecule that is modulated by the protein, where the status of the cell that expresses the protein is modulated. The compositions, proteins, polynucleotides and methods are useful for treating and detecting cancer. The STEAP-1-related proteins are useful for generating cancer vaccines. The polynucleotides are useful as tools for delineating, with greater precision, cytogenetic abnormalities in the chromosomal region that encodes STEAP-1 that may contribute to the malignant phenotype. This is the amino acid sequence of a variant of human six transmembrane epithelial antigen of the prostate or STEAP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                           New composition STEAP-1-related
                                                                                                                                                                                                                                                                                                                                       Faris M,
                                                                                                                                                                                                                                                                                                                                                                                               06-SEP-2001; 2001US-0317840P
05-APR-2002; 2002US-0370387P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine.
                                                                                                                                                                                                                                                                                                       WPI; 2003-313240/30
                                                                                                                                                                                                                             Example 9; Fig 13A; 248pp; English.
 Sequence
                                                                                                                                                                                                                                                                                                                                                                    (AGEN-)
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   339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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   AA;
                                                                                                                                                                                                                                                           comprising a substance that modulates the status of protein, useful for treating and detecting cancer.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                         Challita-Eid
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RESULT 15
ABR54499
ID ABR544499
IX ABR544499
XX ABR54-
XX ABR54-
XX Prost
XX Cytos
XX Immur
X
Search completed: July 12, 2004, 14:07:24 Job time: 33.9651 secs
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                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to novel prostate-specific proteins (PSP) and their coding sequences. The PSPs and their coding sequences are useful for stimulating an immune response in a patient, or for treating prostate cancer in a patient and for determining, detecting or diagnosing the presence of a cancer in a patient. The present sequence was used to illustrate the invention
                                                                                                                                                                                                                                                                                                                                                           Sequence 339 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 5; Page 618-619; 691pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New prostate-specific proteins and genes, useful in gene therapy, particularly for stimulating an immune response in a patient, or treating prostate cancer in a patient, as well as for diagnosing prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA; Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS; Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J; Mcneill PD, Houghton RL, Vinals Y De BassolsC, Foy TM, Watanabe Y; Deng T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-167130/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-MAY-2001; 2001US-00852911.
29-JUN-2001; 2001US-00895814.
10-DEC-2001; 2001US-00012896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-MAY-2002; 2002WO-US014753.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytostatic; gene therapy; prostate-specific protein; PSP; human; immune response; prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prostate tumour specific protein SEQ ID 879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-AUG-2003 (first entry)
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                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                         Conservative
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100.0%; Pr
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                                                                                                                                                                                                                             Score 93; DB 6; Length 339; Pred. No. 1.3e-05; Mismatches 0; Indels
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